STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 178449

TO: Phuong Bui Location: 2a15 / 2c18 Monday, February 06, 2006 Art Unit: 1638 Phone: 571-272-0793 Serial Number: 10 / 733031	From: Jan Delaval Location: Biotech-Chem Library Remsen 1a51 Phone: 571-272-2504 jan.delaval@uspto.gov

Search Notes

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 13:31:14 ; Search time 7523 Seconds
(without alignments)
10676.565 Million cell updates/sec

Title: US-10-733-031-5
Perfect score: 1413
Sequence: 1 aacaccaacaaggcaaccgc.....tggcagcaccactcatcgga 1413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
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6: gb_pat:*
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8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1413	100.0	1413	6	CQ830757	CQ830757 Sequence
2	1413	100.0	1485	6	CQ830758	CQ830758 Sequence
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5	1395.4	98.8	3097	13	AY379742	AY379742 Infectiou
6	1393.8	98.6	3104	13	IPNSEGA	D00701 Infectious
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14	1389	98.3	3097	13	AY374435	AY374435 Infectiou
15	1389	98.3	3097	13	AY379740	AY379740 Infectiou
16	1387.4	98.2	3097	13	AY379737	AY379737 Infectiou
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ALIGNMENTS

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LOCUS CQ830757 1413 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 5 from Patent WO2004055190.
ACCESSION CQ830757
VERSION CQ830757.1 GI:50251037
KEYWORDS .
SOURCE Infectious pancreatic necrosis virus
ORGANISM Infectious pancreatic necrosis virus
Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE 1
AUTHORS Beifuss,K. and Bootland,L.M.
TITLE Immunization of fish with plant-expressed recombinant proteins
JOURNAL Patent: WO 2004055190-A 5 01-JUL-2004;
Novartis AG (CH); Novartis Pharma GmbH (AT); Prodigene, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Infectious pancreatic necrosis virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11002"
ORIGIN

Query Match 100.0%; Score 1413; DB 6; Length 1413;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
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RESULT 2
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DEFINITION  Sequence 6 from Patent WO2004055190.
ACCESSION   CQ830758
VERSION     CQ830758.1  GI:50251038
KEYWORDS    .
SOURCE      Hordeum vulgare
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1
  AUTHORS   Beifuss,K. and Bootland,L.M.
  TITLE     Immunization of fish with plant-expressed recombinant proteins
  JOURNAL   Patent: WO 2004055190-A 6 01-JUL-2004;
            Novartis AG (CH); Novartis Pharma GmbH (AT); Prodigene, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 100.0%; Score 1413; DB 6; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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RESULT 3
AY823632
LOCUS AY823632 3097 bp RNA linear VRL 05-JUL-2005
DEFINITION Infectious pancreatic necrosis virus isolate VP5-deficient Sp103 polyprotein gene, complete cds.
ACCESSION AY823632
VERSION AY823632.1 GI:60550099
KEYWORDS .
SOURCE Infectious pancreatic necrosis virus
ORGANISM Infectious pancreatic necrosis virus
Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE 1 (bases 1 to 3097)
AUTHORS Santi,N., Song,H., Vakharia,V.N. and Evensen,O.
TITLE Infectious Pancreatic Necrosis Virus VP5 Is Dispensable for Virulence and Persistence
JOURNAL J. Virol. 79 (14), 9206-9216 (2005)
PUBMED 15994815
REFERENCE 2 (bases 1 to 3097)
AUTHORS Vakharia,V.N. and Song,H.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-2004) Center for Biosystems Research, University of Maryland Biotechnology Institute, 5115 Plant Sciences Building, College Park, MD 20742, USA
FEATURES Location/Qualifiers
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/virion
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ORIGIN

Query Match 99.1%; Score 1400.2; DB 13; Length 3097;
Best Local Similarity 99.4%; Pred. No. 0;
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Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTATGGGAGGCTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
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Db        422 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

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Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
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Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAACTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
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Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
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Db        782 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Db        842 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
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Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
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Db        962 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
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Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
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Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
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Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1322 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTATAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
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Db       1382 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1441

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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Db       1442 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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RESULT 4
IPA489229
LOCUS       IPA489229              2919 bp    RNA     linear   VRL 11-FEB-2004
DEFINITION  Infectious pancreatic necrosis virus gene for polyprotein, isolate
            88R, genomic RNA.
ACCESSION   AJ489229
VERSION     AJ489229.1  GI:21998737
KEYWORDS    polyprotein.
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1
  AUTHORS   Cutrin,J.M., Barja,J.L., Nicholson,B.L., Bandin,I., Blake,S. and
            Dopazo,C.P.
  TITLE     Restriction Fragment Length Polymorphisms and Sequence Analysis: an
            Approach for Genotyping Infectious Pancreatic Necrosis Virus
            Reference Strains and Other Aquabirnaviruses Isolated from
            Northwestern Spain
  JOURNAL   Appl. Environ. Microbiol. 70 (2), 1059-1067 (2004)
   PUBMED   14766589
REFERENCE   2  (bases 1 to 2919)
  AUTHORS   Cutrin,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-2002) Cutrin J.M., Microbiologia, Virologia,
            Instituto de Acuicultura, USC, Santiago de Compostela, 15706, SPAIN
FEATURES             Location/Qualifiers
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                     /isolate="88R"
                     /specific_host="Oyster"
                     /db_xref="taxon:11002"
     CDS             1. .2919
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                     /db_xref="UniProt/TrEMBL:Q8JK03"
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                     SGGPDGKFSRALKNRLESANYEEVELPPPSKGVIVPVVHTVKSAPGEAFGSLAIIIPG
                     EHPELLDANQQVLSHFANDTGSVWGIGEDIPFEGDNMCYTALPLKEIKRNGNIVVEKI
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ORIGIN

  Query Match           99.0%;  Score 1398.6;  DB 13;  Length 2919;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1404;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
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Db          4 AACACACACAAGGCAACCGCGACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 63

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 123
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Qy       121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
Db       124 AACTTAGAGGTCTCCGAATCAGGAAGTGGAATTCTTGTTTGTTTCCCTGGGGCACCAGGC 183

Qy       181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
Db       184 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 243

Qy       241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
Db       244 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAAGTACGGGAGGCTGATCTCAAGG 303

Qy       301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
Db       304 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 363

Qy       361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
Db       364 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 423

Qy       421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
Db       424 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 483

Qy       481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
Db       484 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 543

Qy       541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
Db       544 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAACTGCACCG 603

Qy       601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
Db       604 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 663

Qy       661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
Db       664 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 723

Qy       721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
Db       724 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 783

Qy       781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
Db       784 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 843

Qy       841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
Db       844 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 903

Qy       901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
Db       904 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 963

Qy       961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
Db       964 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1023

Qy      1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
Db      1024 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1083

Qy      1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
Db      1084 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1143

Qy      1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
Db      1144 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1203

Qy      1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
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Qy      1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
Db      1264 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1323

Qy      1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
Db      1324 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1383

Qy      1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
Db      1384 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1416
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RESULT 5
AY379742

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LOCUS       AY379742               3097 bp    RNA     linear   VRL 16-APR-2004
DEFINITION  Infectious pancreatic necrosis virus isolate NVI-016 segment A 15.4
            kDa non-structural protein and 107 kDa polyprotein genes, complete
            cds.
ACCESSION   AY379742
VERSION     AY379742.1  GI:34559199
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Identification of putative motifs involved in the virulence of
            infectious pancreatic necrosis virus
  JOURNAL   Virology 322 (1), 31-40 (2004)
   PUBMED   15063114
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2003) Department of Pathology, National
            Veterinary Institute, P.O. Box 8156 Dep., Oslo N-0033, Norway
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:11002"
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                     SFSSGNGNVPGVLRPITLVAYEKMTPLSILTVAGVSNYELIPNPELLKNMVTRYGKYD
                     PEGLNYAKMILSHREELDIRTVWRTEEYKERTRVFNEITDFSSDLPTSKAWGWRDIVR
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ORIGIN

  Query Match            98.8%;  Score 1395.4;  DB 13;  Length 3097;
  Best Local Similarity  99.2%;  Pred. No. 0;
  Matches 1402;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        122 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
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Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
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Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
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Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
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Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
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Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
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Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GACGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
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Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGAAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACTTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
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Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
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Db       1202 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
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Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
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Db       1322 ATCCTGTCCCACAGGGAGGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
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Db       1382 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1441

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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Db       1442 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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RESULT 6
IPNSEGA
LOCUS       IPNSEGA                 3104 bp    RNA     linear   VRL 08-MAR-2003
DEFINITION  Infectious pancreatic necrosis virus genes for small ORF, large
            ORF.
ACCESSION   D00701
VERSION     D00701.1  GI:221910
KEYWORDS    major structural polypeptide VP2.
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3104)
  AUTHORS   Havarstein,L.S., Kalland,K.H., Christie,K.E. and Endresen,C.
  TITLE     Sequence of the large double-stranded RNA segment of the N1 strain
            of infectious pancreatic necrosis virus: a comparison with other
            Birnaviridae
  JOURNAL   J. Gen. Virol. 71 (Pt 2), 299-308 (1990)
   PUBMED   2307963
FEATURES             Location/Qualifiers
     source          1. .3104
                     /organism="Infectious pancreatic necrosis virus"
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                     /strain="N1"
                     /db_xref="taxon:11002"
                     /note="5' end of plus-strand segment A."
     CDS             79. .525
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                     /db_xref="GI:221911"
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                     PEGLNYAKMILSHREELDIRTVWRTEEYKERTRVFNEITDFSSDLPTSKAWGWRDIVR
                     GIRKVAAPVLSTLFPMAAPLIGMADQFIGDLTKTNAAGGRYHSMAAGGRHKDVLESWA
                     SGGPDGKFSRALKNRLESANYEEVELPPPSKGVIVPVVHTVKSAPGEAFGSLAIIIPG
                     EYPELLDANQQVLSHFANDTGSVWGIGEDIPFEGDNMCYTALPLKEIKRNGNIVVEKI
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                     PPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFATPEWVALNNYRGPSPGQFKYYL
                     ITGREPEPGDEYEDYIKQPIVKPTDMNKIRRLANSVYGLPHQEPAPEEFYDAVAAVFA
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ORIGIN

  Query Match            98.6%;  Score 1393.8;  DB 13;  Length 3104;
  Best Local Similarity  99.2%;  Pred. No. 0;
  Matches 1401;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
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Db        134 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 193

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
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Db        194 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 253

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
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Db        254 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 313

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Db        314 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 373

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
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Db        374 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 433

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
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Db        434 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 493

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
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Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
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Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Db        614 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 673

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
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Db        734 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 793

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
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Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
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Db        914 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 973

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
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Db        974 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1033

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
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Db       1034 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1093

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
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Db       1094 AACGTCGCCACCCTGGGCACAATGGGTCCGACTACCGTCTCCTTCTCATCAGGGAACGGA 1153

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
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Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              |||||||||||||||||||||||||||||||||||  |  ||||||||||||||||||||
Db       1214 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGTCGTACCCAAACCCAGAACTCCTC 1273

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
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Db       1274 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1333

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
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Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
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Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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Db       1514 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1546


RESULT 7
AY354520
LOCUS       AY354520               3097 bp    RNA     linear   VRL 18-JUL-2005
DEFINITION  Infectious pancreatic necrosis virus isolate Sp116 15-kDa
            nonstructural protein, 108-kDa polyprotein, and 25-kDa
            nonstructural protein genes, complete cds.
ACCESSION   AY354520
VERSION     AY354520.1  GI:38049624
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Shivappa,R.B., Song,H., Yao,K., Aas-Eng,A., Evensen,O. and
            Vakharia,V.N.
  TITLE     Molecular characterization of Sp serotype strains of infectious
            pancreatic necrosis virus exhibiting differences in virulence
  JOURNAL   Dis. Aquat. Org. 61 (1-2), 23-32 (2004)
   PUBMED   15584407
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Vakharia,V.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-2003) Center for Biosystems Research, University
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          of Maryland Biotechnology Institute, 5115 Plant Sciences Building,
          College Park, MD 20742, USA
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match          98.5%;  Score 1392.2;  DB 13;  Length 3097;
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  Matches 1400;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

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Db        122 AACACAAACAAGGCAACCGCAACTTACCTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
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Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
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Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
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Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
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Db        422 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
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Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
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Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
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Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
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Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
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Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
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Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
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Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
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Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
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Db       1322 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1441
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Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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Db       1442 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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Db       1502 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1534


RESULT 8
AY379736
LOCUS       AY379736               3097 bp    RNA     linear   VRL 16-APR-2004
DEFINITION  Infectious pancreatic necrosis virus isolate NVI-020 segment A 15.4
            kDa non-structural protein and 107 kDa polyprotein genes, complete
            cds.
ACCESSION   AY379736
VERSION     AY379736.1  GI:34559183
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Identification of putative motifs involved in the virulence of
            infectious pancreatic necrosis virus
  JOURNAL   Virology 322 (1), 31-40 (2004)
   PUBMED   15063114
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-2003) Department of Pathology, National
            Veterinary Institute, P.O. Box 8156 Dep., Oslo N-0033, Norway
FEATURES             Location/Qualifiers
     source          1. .3097
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                     /codon_start=1
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                     /db_xref="GI:34559184"
                     /translation="MNTNKATATYLKSIMLPETGPASIPDDITERHILKQETSSYNLE
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                     SVLATNDNYRGVSAKMTQSIPTENITKPITRVKLSYKINQQTAIGNAATLGTMGPASV
                     SFSSGNGNVPGVLRPITLVAYEKMTPLSILTVAGVSNYELIPNPELLKNMVTRYGKYD
                     PEGLNYAKMILSHREELDIRTVWRTEEYKERTRVFNEITDFSSDLPTSKAWGWRDIVR
                     GIRKVAAPVLSTLFPMAAPLIGMADQFIGDLTKTNAAGGRYHSMAAGGRHKDVLESWA
                     SGGPDGKFSRALKNRLESANYEEVELPPPSKGVIVPVVHTVKSAPGEAFGSLAIIIPG
                     EYPELLDANQQVLSHFANDTGSVWGIGEDIPFEGDNMCYTALPLKEIKRNGNIVVEKI
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                     ITGREPEPGDEYEDYIKQPIVKPTDMNKIRRLANSVYGLPHQEPAPEEFYDAVAAVFA
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ORIGIN
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 Query Match             98.5%;  Score 1392.2;  DB 13;  Length 3097;
 Best Local Similarity   99.1%;  Pred. No. 0;
 Matches 1400;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
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Db        122 AACACAAACAAGGCAACCGCAACCTACCTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        182 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACAAGAGACCTCGTCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
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Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
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Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
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Db        422 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
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Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
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Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
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Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTACTGCGACAGGAACC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
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Db        782 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACGACAGTGACGGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Db        842 ATAAACTTCAGTCTGGCAGAACAACCCGCAGTCGAGACCAAGTTCGACTTCCAGCTGGAC 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
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Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
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Db        962 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
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Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
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Db       1082 AACGCCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141
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Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
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Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
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Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
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Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
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Db       1382 GAGAGGACCAGAGTCTTCAATGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1441

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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RESULT 9
AY379744
LOCUS       AY379744               3097 bp    RNA     linear   VRL 16-APR-2004
DEFINITION  Infectious pancreatic necrosis virus isolate NVI-010 segment A 107
            kDa polyprotein gene, complete cds.
ACCESSION   AY379744
VERSION     AY379744.1  GI:34559204
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Identification of putative motifs involved in the virulence of
            infectious pancreatic necrosis virus
  JOURNAL   Virology 322 (1), 31-40 (2004)
   PUBMED   15063114
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-2003) Department of Pathology, National
            Veterinary Institute, P.O. Box 8156 Dep., Oslo N-0033, Norway
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:11002"
                     /segment="A"
     CDS             119. .3037
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                     SVLATNDNYRGVSAKMTQSIPTENITKPITRVKLSYKINQQTAIGNVATLGTMGPASV
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ORIGIN
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  Query Match            98.5%;  Score 1392.2;  DB 13;  Length 3097;
  Best Local Similarity  99.1%;  Pred. No. 0;
  Matches 1400;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
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Db        122 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
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Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
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Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
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Db        422 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
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Db        482 AACGCTGCCACCTTTGAAGGCAGCCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
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Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAGCGCCTACCCCCCGTTCCTGCGATAGGAACC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
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Db        782 CTCACCACTCTCTATGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Db        842 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
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Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
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Db        962 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960

Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020

Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

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Db       1322 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320

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Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380

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Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413

Db       1502 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1534


RESULT 10
AR164547
LOCUS       AR164547               3097 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 38 from patent US 6274147.
ACCESSION   AR164547
VERSION     AR164547.1  GI:16237602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Vakharia,V.N. and Yao,K.
  TITLE     Method for generating nonpathogenic infectious pancreatic necrosis
            virus (IPNV) from synthetic RNA transcripts
  JOURNAL   Patent: US 6274147-A 38 14-AUG-2001;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             98.4%;  Score 1390.6;  DB 6;  Length 3097;
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Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120

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Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360

Db        422 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420

Db        482 AACGCTGCCACCTTCGAGGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480

Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540

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Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660

Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGGGCC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720

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Db        842 ATAAACTTCAGTCTGGCAGAACAACCCGCAGTCGAGACCAAGTTCGACTTCCAGCTGGAC 901

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Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900

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Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020

Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080

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Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

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Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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Db       1502 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1534


RESULT 11
AY354521
LOCUS       AY354521               3097 bp    RNA     linear   VRL 18-JUL-2005
DEFINITION  Infectious pancreatic necrosis virus isolate Sp122 12-kDa
            nonstructural protein, 108-kDa polyprotein, and 25-kDa
            nonstructural protein genes, complete cds.
ACCESSION   AY354521
VERSION     AY354521.1  GI:38049628
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Shivappa,R.B., Song,H., Yao,K., Aas-Eng,A., Evensen,O. and
            Vakharia,V.N.
  TITLE     Molecular characterization of Sp serotype strains of infectious
            pancreatic necrosis virus exhibiting differences in virulence
  JOURNAL   Dis. Aquat. Org. 61 (1-2), 23-32 (2004)
   PUBMED   15584407
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Vakharia,V.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-2003) Center for Biosystems Research, University
            of Maryland Biotechnology Institute, 5115 Plant Sciences Building,
            College Park, MD 20742, USA
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             98.4%;  Score 1390.6;  DB 13;  Length 3097;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1399;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
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Db        122 AACACAAACAAGGCAACCGCAACTTACCTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
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Db        182 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACAAGAGACCTCGTCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
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Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
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Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AAATATGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
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Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
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Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
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Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
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Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
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Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
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Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
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Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
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Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
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RESULT 12
AY379735
LOCUS       AY379735               3097 bp    RNA     linear   VRL 16-APR-2004
DEFINITION  Infectious pancreatic necrosis virus isolate NVI-011 segment A 14.7
            kDa non-structural protein and 107 kDa polyprotein genes, complete
            cds.
ACCESSION   AY379735
VERSION     AY379735.1  GI:34559180
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Identification of putative motifs involved in the virulence of
            infectious pancreatic necrosis virus
  JOURNAL   Virology 322 (1), 31-40 (2004)
   PUBMED   15063114
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-2003) Department of Pathology, National
            Veterinary Institute, P.O. Box 8156 Dep., Oslo N-0033, Norway
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           98.4%;  Score 1390.6;  DB 13;  Length 3097;
  Best Local Similarity 99.0%;  Pred. No. 0;
  Matches 1399;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

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Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 421

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Db        422 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              ||||||||||||| |||||||| |||||||||| |||||||||||||||||||||||||
Db        482 AACGCTGCCACCTTTGAAGGCAGCCTGTCTGAGGTAGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
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Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540

Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600

Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660

Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTACTGCGACAGGAACC 781

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Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780

Db        842 ATAAACTTCAGTCTGGCAGAACAACCCGCAGTCGAGACCAAGTTCGACTTCCAGCTGGAC 901

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Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

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Db        962 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960

Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

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Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

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Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140

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Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260

Db       1322 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1381

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Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380

Db       1442 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCCGTACTGTCC 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413

Db       1502 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1534


RESULT 13
AY354519
LOCUS       AY354519               3097 bp    RNA     linear   VRL 18-JUL-2005
DEFINITION  Infectious pancreatic necrosis virus isolate Sp103 15-kDa
            nonstructural protein, 108-kDa polyprotein, and 25-kDa
            nonstructural protein genes, complete cds.
ACCESSION   AY354519
VERSION     AY354519.1  GI:38049606
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Shivappa,R.B., Song,H., Yao,K., Aas-Eng,A., Evensen,O. and
            Vakharia,V.N.
  TITLE     Molecular characterization of Sp serotype strains of infectious
            pancreatic necrosis virus exhibiting differences in virulence
  JOURNAL   Dis. Aquat. Org. 61 (1-2), 23-32 (2004)
   PUBMED   15584407
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Shivappa,R., Song,H., Yao,K. and Vakharia,V.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-2003) Center for Biosystems Research, University
            of Maryland Biotechnology Institute, 5115 Plant Sciences Building,
            College Park, MD 20742, USA
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             98.3%;  Score 1389;  DB 13;  Length 3097;
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Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
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Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
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Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGTTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
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Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGGGCC 781

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Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
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Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
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Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
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Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
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Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
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Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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RESULT 14
AY374435
LOCUS       AY374435               3097 bp    RNA     linear   VRL 16-APR-2004
DEFINITION  Infectious pancreatic necrosis virus isolate NVI-001 segment A 15.4
            kDa non-structural protein and 107 kDa polyprotein genes, complete
            cds.
ACCESSION   AY374435
VERSION     AY374435.1  GI:34559206
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Identification of putative motifs involved in the virulence of
            infectious pancreatic necrosis virus
  JOURNAL   Virology 322 (1), 31-40 (2004)
   PUBMED   15063114
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-2003) Department of Pathology, National
            Veterinary Institute, P.O. Box 8156 Dep., Oslo N-0033, Norway
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           98.3%;  Score 1389;  DB 13;  Length 3097;
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Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
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Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
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Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
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Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
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Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
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Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
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Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
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Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
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Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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RESULT 15
AY379740
LOCUS       AY379740               3097 bp    RNA     linear   VRL 16-APR-2004
DEFINITION  Infectious pancreatic necrosis virus isolate NVI-015 segment A 12.1
            kDa non-structural protein and 107 kDa polyprotein genes, complete
            cds.
ACCESSION   AY379740
VERSION     AY379740.1  GI:34559194
KEYWORDS    .
SOURCE      Infectious pancreatic necrosis virus
  ORGANISM  Infectious pancreatic necrosis virus
            Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
REFERENCE   1  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Identification of putative motifs involved in the virulence of
            infectious pancreatic necrosis virus
  JOURNAL   Virology 322 (1), 31-40 (2004)
   PUBMED   15063114
REFERENCE   2  (bases 1 to 3097)
  AUTHORS   Santi,N., Vakharia,V.N. and Evensen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-2003) Department of Pathology, National
            Veterinary Institute, P.O. Box 8156 Dep., Oslo N-0033, Norway
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 98.3%; Score 1389; DB 13; Length 3097;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1398; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
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Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
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Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
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Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
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Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
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Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
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Job time : 7527 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 13:47:00 ; Search time 6251 Seconds
(without alignments)
10575.931 Million cell updates/sec

Title: US-10-733-031-5
Perfect score: 1413
Sequence: 1 aacaccaacaaggcaaccgc.....tggcagcaccactcatcgga 1413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	55.2	3.9	591	3	BM613888	BM613888 170006871
	2	55.2	3.9	685	3	BM611283	BM611283 170006871
	3	55.2	3.9	706	3	BM651894	BM651894 170006873
c	4	47	3.3	854	9	AQ743932	AQ743932 HS_5504_A
c	5	46.4	3.3	1101	10	CNS014Y2	AL104756 Drosophil
c	6	45	3.2	922	10	CNS0073W	AL066784 Drosophil
	7	44.8	3.2	551	10	CL821568	CL821568 OR_CBa004
	8	44.8	3.2	604	6	CA756299	CA756299 BR0300390
	9	44.8	3.2	633	5	BX478954	BX478954 DKFZp686C
	10	44.8	3.2	983	8	CX099848	CX099848 RECm0607
	11	44.8	3.2	3939	11	DQ038218	DQ038218 Homo sapi
c	12	43.8	3.1	1074	11	CNS06TFB	AL414477 T7 end of
c	13	43.4	3.1	895	10	CNS0071A	AL066286 Drosophil
	14	43.2	3.1	465	10	CL746019	CL746019 OR_BBa008
	15	43.2	3.1	582	10	CL736300	CL736300 OR_BBa007
c	16	43	3.0	884	10	CNS006U0	AL065923 Drosophil
	17	42.4	3.0	636	6	CF306483	CF306483 HDA1--03-
	18	42.4	3.0	858	10	CL963368	CL963368 OsIFCC009
c	19	42.4	3.0	914	10	CNS00CZP	AL059740 Drosophil
	20	42.4	3.0	1101	10	CNS017SY	AL108460 Drosophil
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c	22	41.8	3.0	483	9	CC063988	CC063988 fgma003d0
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	24	41.8	3.0	992	1	AL554541	AL554541 AL554541
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	34	41	2.9	438	2	BG013927	BG013927 IL5-GN024
	35	41	2.9	518	2	BG770817	BG770817 602719002
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	40	40.6	2.9	432	3	BJ248153	BJ248153 BJ248153
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	42	40.6	2.9	827	8	CV780755	CV780755 FGAS07516
	43	40.4	2.9	475	8	DN257366	DN257366 Meso08098
	44	40.4	2.9	620	8	DN257520	DN257520 Meso08107
	45	40.4	2.9	864	7	CJ415620	CJ415620 CJ415620

ALIGNMENTS

RESULT 1
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LOCUS BM613888 591 bp mRNA linear EST 25-FEB-2002
DEFINITION 17000687140349 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449679799 5', mRNA sequence.
ACCESSION BM613888
VERSION BM613888.1 GI:18911994
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.
REFERENCE 1 (bases 1 to 591)
AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
TITLE Celera Anopheles gambiae EST project
JOURNAL Unpublished (2002)
COMMENT Contact: Holt R.A.
Celera Genomics
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU01004B44 row: O column: 17
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .591
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/mol_type="mRNA"
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/db_xref="taxon:7165"
/clone="19600449679799"
/dev_stage="Adult"
/lab_host="DH10b"
/clone_lib="A.Gam.ad.cDNA.blood1"
/note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"
ORIGIN

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  Query Match             3.9%;  Score 55.2;  DB 3;  Length 591;
  Best Local Similarity   50.4%;  Pred. No. 0.0014;
  Matches  135;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy        713 CGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCC 772
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Db        217 CGGGCATGCTGAAGTTTATCGGCGAAACGCAGTTCGCCAGCGGCACCTGGTGCGGCGTCC 276

Qy        773 AGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGC 832
              ||||||||     | ||    | ||||||| | | || | |    ||       || || |
Db        277 AGCTGGACGAGGCGAGCGGCAAGAACGACGGCACGGTGGACGGTGTCAGATACTTCGAGT 336

Qy        833 TGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCG 892
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Db        337 GTCCGGCCAAGTACGGCATCTTTGTGCCGATTGCCAAGGTGACGCTGTCCCCGTCGGCCC 396

Qy        893 AGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAG 952
              || | | |    | | |  || ||| |||   |     |   | ||||   || | |
Db        397 GCAAAACCTCGGCCCGGCTGTCCCGGGCCAACTCGAAGGAGTCGCTCAATTCGCTGGCCA 456

Qy        953 CAATCGGCAACGTCGCCACCCTGGGCAC 980
              | ||  ||    |||| |||  || |||
Db        457 CGATGAGCTCGATCGCGACCACGGCCAC 484


RESULT 2
BM611283
LOCUS       BM611283                685 bp    mRNA    linear   EST 25-FEB-2002
DEFINITION  17000687114520 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
            19600449690651 5', mRNA sequence.
ACCESSION   BM611283
VERSION     BM611283.1  GI:18909387
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 685)
  AUTHORS   Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
            Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
  TITLE     Celera Anopheles gambiae EST project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Holt R.A.
            Celera Genomics
            45 w. Gude Dr., Rockville, MD 20850, USA
            Tel: 2404533151
            Fax: 2404534580
            Email: HoltRA@celera.com
            Plate: NU01004AZ1  row: C  column: 21
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:7165"
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                     /lab_host="DH10b"
                     /clone_lib="A.Gam.ad.cDNA.blood1"
                     /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole
                     adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
                     hours  after human blood feeding. cDNA inserts >500 bp
                     cloned directionally  into pSport 1. Not 1 site is 3'.
                     Clones available through the Malaria  Research and
                     Reference Reagent Resource Center (www.malaria.mr4.org)"
ORIGIN

  Query Match             3.9%;  Score 55.2;  DB 3;  Length 685;
  Best Local Similarity   50.4%;  Pred. No. 0.0014;
  Matches  135;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

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              ||||     | || || |     | |   ||   ||| | ||  |||  || || | |||
Db         63 CGGGCATGCTGAAGTTTATCGGCGAAACGCAGTTCGCCAGCGGCACCTGGTGCGGCGTCC 122

Qy        773 AGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGC 832
              ||||||||     | ||    | ||||||| | | || | |    ||       || || |
Db        123 AGCTGGACGAGGCGAGCGGCAAGAACGACGGCACGGTGGACGGTGTCAGATACTTCGAGT 182

Qy        833 TGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCG 892
              |  | ||  ||  | |   |        ||||| |||| | ||||    || ||
Db        183 GTCCGGCCAAGTACGGCATCTTTGTGCCGATTGCCAAGGTGACGCTGTCCCCGTCGGCCC 242

Qy        893 AGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAG 952
              || | | |    | | |  || ||| |||   |     |   | ||||   || | |
Db        243 GCAAAACCTCGGCCCGGCTGTCCCGGGCCAACTCGAAGGAGTCGCTCAATTCGCTGGCCA 302

Qy        953 CAATCGGCAACGTCGCCACCCTGGGCAC 980
              | ||  ||    |||| |||  || |||
Db        303 CGATGAGCTCGATCGCGACCACGGCCAC 330


RESULT 3
BM651894
LOCUS       BM651894                706 bp    mRNA    linear   EST 26-FEB-2002
DEFINITION  17000687374836 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
            19600449665488 5', mRNA sequence.
ACCESSION   BM651894
VERSION     BM651894.1  GI:18951405
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 706)
  AUTHORS   Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
            Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
  TITLE     Celera Anopheles gambiae EST project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Holt R.A.
            Celera Genomics
            45 w. Gude Dr., Rockville, MD 20850, USA
            Tel: 2404533151
            Fax: 2404534580
            Email: HoltRA@celera.com
            Plate: NU01004I89  row: K  column: 22
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .706
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="RSP-ST (Reduced susc. to Permethrin - std.
                     chromosome)"
                     /db_xref="taxon:7165"
                     /clone="19600449665488"
                     /dev_stage="Adult"
                     /lab_host="DH10b"
                     /clone_lib="A.Gam.ad.cDNA1"
                     /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole
                     adult mosquitoes (mixed sex) frozen on liquid nitrogen.
                     cDNA  inserts >500 bp cloned directionally into pSport 1.
                     Not 1 site is  3'. Clones available through the Malaria
                     Research and Reference  Reagent Resource Center
                     (www.malaria.mr4.org)."
ORIGIN

  Query Match             3.9%;  Score 55.2;  DB 3;  Length 706;
  Best Local Similarity   50.4%;  Pred. No. 0.0015;
  Matches  135;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy        713 CGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCC 772
              ||||     | || || |     | |   ||   ||| | ||  |||  || || | |||
```

```
Db        312 CGGGCATGCTGAAGTTTATCGGCGAAACGCAGTTCGCCAGCGGCACCTGGTGCGGCGTCC 371

Qy        773 AGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGC 832
              ||||||||     | ||    | |||||||| | | || | |    ||       || || |
Db        372 AGCTGGACGAGGCGAGCGGCAAGAACGACGGCACGGTGGACGGTGTCAGATACTTCGAGT 431

Qy        833 TGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCG 892
                | | ||  ||  |  |    |         |||||| |||| | ||||    || ||
Db        432 GTCCGGCCAAGTACGGCATCTTTGTGCCGATTGCCAAGGTGACGCTGTCCCCGTCGGCCC 491

Qy        893 AGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAG 952
                || | |     | | |  || ||| |||   |    |   | ||||   || | |
Db        492 GCAAAACCTCGGCCCGGCTGTCCCGGGCCAACTCGAAGGAGTCGCTCAATTCGCTGGCCA 551

Qy        953 CAATCGGCAACGTCGCCACCCTGGGCAC 980
              | ||  ||    |||| |||  || |||
Db        552 CGATGAGCTCGATCGCGACCACGGCCAC 579
```

RESULT 4
AQ743932/c
LOCUS AQ743932 854 bp DNA linear GSS 16-JUL-1999
DEFINITION HS_5504_A1_A11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1080 Col=21 Row=A, genomic survey sequence.
ACCESSION AQ743932
VERSION AQ743932.1 GI:5521454
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 854)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1080 row: A column: 21
Seq primer: T7
Class: BAC ends
High quality sequence stop: 854.
FEATURES Location/Qualifiers
source 1. .854
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1080 Col=21 Row=A"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
ORIGIN

Query Match 3.3%; Score 47; DB 9; Length 854;
Best Local Similarity 52.9%; Pred. No. 0.27;
Matches 101; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```
Qy        589 GCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCT 648
              | ||  |   || |||| | || |  |    |||| | |||  ||| | |||    |||
Db        261 GGAAAGGTCACGTGGAGCTGGGAAAAAGTGGACCCAGCACAATACCTCCTCCCACCCCCT 202

Qy        649 GCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACA 708
              | || ||||||||||||  ||     |   ||| ||  |    | |  ||     | || |
Db        201 GGGAAAGGAACCCTCAATACAAGTTGTCAGGCAACAACTCTTAACTACATTCTAAAAATA 142

Qy        709 GTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGAC 768
              |||  |  | |  ||| || || | |   | |||    |||  || |  || |   |
Db        141 TTGATGTAAAATTTAATCTCCATTTTTAGAAGAAAACAATGAAAAAAGGCATAGATGTGC 82

Qy        769 TTCCAGCTGGA 779
                | | |||| |
Db         81 ATACTGCTGCA 71
```

RESULT 5
CNS014Y2/c
LOCUS CNS014Y2 1101 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN12I13 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL104756
VERSION AL104756.1 GI:5616770
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN12I13"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
ORIGIN

Query Match 3.3%; Score 46.4; DB 10; Length 1101;
Best Local Similarity 19.5%; Pred. No. 0.42;
Matches 64; Conservative 149; Mismatches 115; Indels 1; Gaps 1;

```
Qy        438 CCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACC 497
              :::::| |::::::  : ::: ::::  | :: :::::|:|  ::|  ::  ::   :::
Db       1099 VMMMMAMGMVMVMSGGMGMMVGMVVVVMGGVMGMVMVVGMGMGMVAMMVMGMMMCGMVVM 1040

Qy        498 AACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACACCCCAGGGTCTCCAGTC 557
              :::::|   :: : ::::: ::: :||:: : :| :: :::::::: |:|  : :::
Db       1039 MMMMVGMMCMVGMSVVMMMVMVVNMCGMMGMMVGMMVMMVMVMMVVNAVGMGMAVMVAMA 980

Qy        558 AATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGA 617
               :  ::::|:|:: :|| |: | |:::  | |:    | : :|::::::   :  : | :
```

```
Db        979 GMMMVVMVGVGMV-MGAMGVMGVGVVVGMCVGVGGMGGGVNVGMVRMVVMGGSGMVCCAM 921

Qy        618 CCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGA 677
              | ||:  | |  ||:| ::||| |      |||:| ::::     :|  : :     |:
Db        920 ACSCCMCSCACCGCGVCGMYCCCRCCCCGAAGCGVCCVVMVTGTGGVCRGVGVGGRGGGD 861

Qy        678 GGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGC 737
              ::|:::|:||:  : |  |: : :|:|::::: :| |:: : :: ::|   : | | |::
Db        860 KVGVVMCRCCSGAMCCCCCMCMCVCMCMVVVVVVARGVVGRCMVMMMARMVSGGMCCGSV 801

Qy        738 AGAACAACCCGCAAACGAGACCAAGTTCG 766
              | |: : :|||: :  ::: |: :|  :|
Db        800 ACAMGMGVCCGSGMCGVRVCCSGMGGSVG 772


RESULT 6
CNS0073W/c
LOCUS       CNS0073W                922 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL066784
VERSION     AL066784.1  GI:4945247
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 922)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .922
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR14D09"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             3.2%;  Score 45;  DB 10;  Length 922;
  Best Local Similarity   18.0%;  Pred. No. 0.97;
  Matches   54;  Conservative  115;  Mismatches  131;  Indels    0;  Gaps    0;

Qy        617 ACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACG 676
              :|: |||: |||  :: |:  :::|:|   ::  : :|:  ::|:| |:::::  :   ||
Db        918 MCMMCCCMCCCCCMMMCMMCMMMCMCCMCMMMCMMMCMMMMMCMCMCMMMMMMMMACACA 859

Qy        677 AGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGG 736
              :   : ::  | ::: :  |::  ||::| ::   |:   : ::| :|:|  :|  :
Db        858 MMAAMNMMMACMMMCMMACMMAMCCMMACMMMAMAMMMMMMMAMMAMCACMAMMMACA 799

Qy        737 CAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACA 796
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              |: |::::|:: ::::: :  :: :   | ::   |: :   :|  |:    |:   : |
Db        798 CMCAMMMMCMMMMMMMMCMMCMMCMCCACMMMACACMAMCCMMCMMCMMACMCMMAAMAA 739

Qy        797 ACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAG 856
              :: :   :: :      :: :      :   ::   :   :| :||:  |::|| :|:
Db        738 MMMMACAMMAMAAMMMMMAMAAMMAAMMAAMMMMAMMCCMCCMAAMAMAMMACMMCMMCA 679

Qy        857 GAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCA 916
                :  : || :::: :  :::|    || :|: ||: : :| : ::::|  :: :  |::|
Db        678 MMMMMMCAMMMMAMMAMMMCCCAACAMMCMCACMMMCMAAMAMMMMACMMMAMMAAMMA 619


RESULT 7
CL821568
LOCUS       CL821568                551 bp    DNA     linear   GSS 09-AUG-2004
DEFINITION  OR_CBa0040I20.r OR_CBa Oryza rufipogon genomic clone OR_CBa0040I20
            3', genomic survey sequence.
ACCESSION   CL821568
VERSION     CL821568.1  GI:51067178
KEYWORDS    GSS.
SOURCE      Oryza rufipogon
  ORGANISM  Oryza rufipogon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
            Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
            Wing,R.
  TITLE     OMAP project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0040  row: I  column: 20
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .551
                     /organism="Oryza rufipogon"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4529"
                     /clone="OR_CBa0040I20"
                     /tissue_type="young leaves"
                     /dev_stage="2 week old seedlings"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="OR_CBa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
                     drk treated 36 hrs before harvest"
ORIGIN

  Query Match             3.2%;  Score 44.8;  DB 10;  Length 551;
  Best Local Similarity   49.3%;  Pred. No. 0.97;
  Matches  146;  Conservative    0;  Mismatches  147;  Indels    3;  Gaps    1;

Qy        751 AACGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTT 810
              | | |  |||  | ||| | |||| |    | ||  |  ||| ||| ||| | |||| |
Db        163 AGCAACCCCATCTGCGAGTCCCAGGTCATCGTCCAGTACCTCGACGACGCCTTCCCCGGC 222

Qy        811 GTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAG 870
              | | | |  | | ||  | | ||  || | |  | ||  | | |  ||| |
Db        223 GGCGCCGCCGGCGGCGACCTCCTCCCCTCCGACCCCCACGCCCGCGCCGTCGCCCGATTC 282

Qy        871 ATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCA 930
                | |   || ||||    |||||  | || |   |  || ||    | || |   | |
Db        283 TGGGCGGCGTACATCGACGCCGAGTTCTTCGCGCCGTGGAACAGGTCGTTCTACACGGCG 342
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Qy        931 TACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACC---CTGGGCACAATGGGT 987
              |   ||     |  ||  | | |  || || |  |  ||  |    ||||  || || |
Db        343 TCGGAGGAGGAGAAGACGGCGGAGATGGGGAGGGCGGCGGCGGCGCTGGCGACGATCGAG 402

Qy        988 CCAGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACC 1043
              |  || | ||       | ||    ||||| ||     || |||||| |  ||| ||
Db        403 CGCGCGTTCGCGGAGCTGTCGAGGGGGAAGGGGTTCTTCTCCGGCGAGGACAGGCC 458


RESULT 8
CA756299
LOCUS       CA756299                604 bp    mRNA    linear   EST 27-NOV-2002
DEFINITION  BR030039000_PLATE_G02_15_018.ab1 OA Oryza sativa (japonica
            cultivar-group) cDNA clone BR030039000_PLATE_G02_15_018.ab1 similar
            to (AF244705) glutathione S-transferase GST 40 [Zea mays], mRNA
            sequence.
ACCESSION   CA756299
VERSION     CA756299.1  GI:25800338
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 604)
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Mark Fredricksen
            Department of Plant Biology
            University of Illinois
            1201 W. Gregory Dr., Urbana, IL 61801, USA
            Tel: 2172655473
            Email: bohnertlab@life.uiuc.edu.
FEATURES             Location/Qualifiers
     source          1. .604
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="BR030039000_PLATE_G02_15_018.ab1"
                     /tissue_type="roots"
                     /dev_stage="3-4 weeks"
                     /clone_lib="OA"
                     /note="19 h 200mM NaCl"
ORIGIN

  Query Match             3.2%;  Score 44.8;  DB 6;  Length 604;
  Best Local Similarity   49.3%;  Pred. No. 0.99;
  Matches  146;  Conservative    0;  Mismatches  147;  Indels    3;  Gaps    1;

Qy        751 AACGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTT 810
              | | |  |||  | ||| | |||| |   | ||  |  ||| ||| ||| | ||||
Db        224 AGCAACCCCATCTGCGAGTCCCAGGTCATCGTCCAGTACCTCGACGACGCCTTCCCCGGC 283

Qy        811 GTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAG 870
              | | | |  | | ||  | | ||  || |  |   | ||  | | |  ||| |
Db        284 GGCGCCGCCGGCGGCGACCTCCTCCCCTCCGACCCCCACGCCCGCGCCGTCGCCCGATTC 343

Qy        871 ATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCA 930
                | |   || ||||    |||||  | || |   |  || ||     | ||| |   | |
Db        344 TGGGCGGCGTACATCGACGCCGAGTTCTTCGCGCCGTGGAACAGGTCGTTCTACACGGCG 403

Qy        931 TACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACC---CTGGGCACAATGGGT 987
              |   ||     |  ||  | | |  || || |  |  ||  |    ||||  || || |
Db        404 TCGGAGGAGGAGAAGACGGCGGAGATGGGGAGGGCGGCGGCGGCGCTGGCGACGATCGAG 463

Qy        988 CCAGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACC 1043
              |  || | ||       | ||    ||||| ||     || |||||| |  ||| ||
Db        464 CGCGCGTTCGCGGAGCTGTCGAGGGGGAAGGGGTTCTTCTCCGGCGAGGACAGGCC 519


RESULT 9
BX478954
LOCUS       BX478954                633 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686C06208_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686C06208 5', mRNA sequence.
ACCESSION   BX478954
VERSION     BX478954.1  GI:31914270
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686C06208) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686C06208"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

  Query Match             3.2%;  Score 44.8;  DB 5;  Length 633;
  Best Local Similarity   50.5%;  Pred. No. 1;
  Matches  109;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy        634 CTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACATC 693
              ||  ||  || ||  |     |  || |||  |||  || | |     | | |||  | |
Db        316 CTGGCCAGCGCTCTGGACTACGAGACACTCTACACATTCAAAGTCACCATCTCCGTGAGC 375

Qy        694 GTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAAC 753
              | |  || ||      |||  | | || ||      | | | ||| |||    |  ||  |||
Db        376 GACCCCTACATCCAGGTGCAGAGGGAGATGCTGGTGATTGTGGAAGATAGAAACGACAAC 435

Qy        754 GAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGTC 813
              |   ||   ||| |   |          || ||   || |  || |   | | || || | |
Db        436 GCACCCGTTTTCCAGAACACCGCTTTCTCCACCAGCATCAACGAGACCCTGCCCGTGGGC 495

Qy        814 ACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAAC 849
              |  |||||   |||||||||||||    || |  ||
Db        496 AGTGTGGTGTTCTCCGTGCTGGCCGTGGATAAAGAC 531


RESULT 10
CX099848
LOCUS       CX099848                983 bp    mRNA    linear   EST 03-JUN-2005
DEFINITION  RECm0607 A normalized whole-life-cycle cDNA library of rice Oryza
            sativa (indica cultivar-group) cDNA clone BI073K05, BI145M10 5',
            mRNA sequence.
ACCESSION   CX099848
```

```
VERSION     CX099848.1  GI:66913000
KEYWORDS    EST.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan,D.,
            Han,B., Zhang,Q. and Wang,S.
  TITLE     Features of the expressed sequences revealed by a large-scale
            analysis of ESTs from a normalized cDNA library of the elite indica
            rice cultivar Minghui 63
  JOURNAL   Plant J. 42 (5), 772-780 (2005)
   PUBMED   15918889
COMMENT     Contact: Wang S
            National Key Laboratory of Crop Genetic Improvement
            Hauzhong Agricultural University
            Wuhan 430070, China
            Tel: 86-27-87282044
            Fax: 86-27-87287092
            Email: shipingwang@hotmail.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .983
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="mRNA"
                     /strain="indica"
                     /cultivar="Minghui 63"
                     /db_xref="taxon:39946"
                     /clone="BI073K05, BI145M10"
                     /tissue_type="whole plant"
                     /dev_stage="whole-life-cycle"
                     /lab_host="E. coli DH10B"
                     /clone_lib="A normalized whole-life-cycle cDNA library of
                     rice"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; The
                     library is constructed based on the strategy of satuation
                     hybridization with genomic DNA using rice cultivar Minghui
                     63. This library consists of cDNA from 15 directionally
                     cloned cDNA libraries constructed with different tissues
                     from 9 developmental stages."
ORIGIN

  Query Match             3.2%;  Score 44.8;  DB 8;  Length 983;
  Best Local Similarity   49.3%;  Pred. No. 1.1;
  Matches  146;  Conservative    0;  Mismatches  147;  Indels    3;  Gaps    1;

Qy        751 AACGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTT 810
              | | |  |||  | ||| | ||||  |    | ||  |  ||| ||| ||| | ||||
Db        266 AGCAACCCCATCTGCGAGTCCCAGGTCATCGTCCAGTACCTCGACGACGCCTTCCCCGGC 325

Qy        811 GTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAG 870
              | | | |  | | ||  | | ||  || |  |  | ||  | | |  ||| |
Db        326 GGCGCCGCCGGCGGCGACCTCCTCCCCTCCGACCCCCACGCCCGCGCCGTCGCCCGATTC 385

Qy        871 ATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCA 930
                | |   || ||||    |||||  | || |  |  || ||   | || |   | |
Db        386 TGGGCGGCGTACATCGACGCCGAGTTCTTCGCGCCGTGGAACAGGTCGTTCTACACGGCG 445

Qy        931 TACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACC---CTGGGCACAATGGGT 987
              |   ||     |  ||  | | |  || || |  |  ||  |    ||||  || || |
Db        446 TCGGAGGAGGAGAAGACGGCGGAGATGGGGAGGGCGGCGGCGGCGCTGGCGACGATCGAG 505

Qy        988 CCAGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACC 1043
              |  || | ||       | ||    ||||| ||      || |||||| |  ||| ||
Db        506 CGCGCGTTCGCGGAGCTGTCGAGGGGGAAGGGGTTCTTCTCCGGCGAGGACAGGCC 561


RESULT 11
DQ038218
LOCUS       DQ038218               3939 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Homo sapiens PC-LKC gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ038218
VERSION     DQ038218.1  GI:66889427
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3939)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 3939)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .3939
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
     gene            <1. .>3939
                     /gene="PC-LKC"
                     /locus_tag="HC8007"
ORIGIN

  Query Match             3.2%;  Score 44.8;  DB 11;  Length 3939;
  Best Local Similarity   50.5%;  Pred. No. 1.6;
  Matches  109;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy        634 CTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACATC 693
              ||  ||  || ||  |     |  || |||  |||  || | |     | | |||  | |
Db        241 CTGGCCAGCGCTCTGGACTACGAGACACTCTACACATTCAAAGTCACCATCTCCGTGAGC 300

Qy        694 GTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAAC 753
              | |  || ||      |||  | | || ||      | | | ||| |||   |  ||  |||
Db        301 GACCCCTACATCCAGGTGCAGAGGGAGATGCTGGTGATTGTGGAAGATAGAAACGACAAC 360

Qy        754 GAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGTC 813
              |  ||  ||| |   |      || ||   || |  || |   | | || || | |
Db        361 GCACCCGTTTTCCAGAACACCGCTTTCTCCACCAGCATCAACGAGACCCTGCCCGTGGGC 420

Qy        814 ACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAAC 849
              |  |||||   ||||||||||||||    || |  ||
Db        421 AGTGTGGTGTTCTCCGTGCTGGCCGTGGATAAAGAC 456


RESULT 12
CNS06TFB/c
LOCUS       CNS06TFB               1074 bp    DNA     linear   GSS 05-JUL-2001
DEFINITION  T7 end of clone AW0AA031B09 of library AW0AA from strain CLIB 89 of
            Yarrowia lipolytica, genomic survey sequence.
ACCESSION   AL414477
VERSION     AL414477.1  GI:12187722
KEYWORDS    GSS.
SOURCE      Yarrowia lipolytica
  ORGANISM  Yarrowia lipolytica
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Dipodascaceae; Yarrowia.
REFERENCE   1  (bases 1 to 1074)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
```

Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 11152876
REFERENCE 2 (bases 1 to 1074)
AUTHORS Casaregola,S., Neuveglise,C., Lepingle,A., Bon,E., Feynerol,C., Artiguenave,F., Wincker,P. and Gaillardin,C.
TITLE Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia lipolytica
JOURNAL FEBS Lett. 487 (1), 95-100 (2000)
PUBMED 11152892
REFERENCE 3 (bases 1 to 1074)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
FEATURES Location/Qualifiers
source 1. .1074
/organism="Yarrowia lipolytica"
/mol_type="genomic DNA"
/strain="CLIB 89"
/db_xref="taxon:4952"
/clone="AW0AA031B09"
/clone_lib="AW0AA"
/note="end : T7"
ORIGIN

Query Match 3.1%; Score 43.8; DB 11; Length 1074;
Best Local Similarity 52.5%; Pred. No. 2.2;
Matches 96; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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Qy        745 CCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTC 804
              ||| ||| |   | |||  |   ||||| ||| |||||||  |  | |      || | |
Db        425 CCCCCAACCACCATCAAAATGTCCTTCCCGCTCGACTTCAAGTACGTCATTGCCGCCACC 366

Qy        805 CCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCA 864
                |  |   | | ||  |  ||| | | | | ||   |||     |||| |  ||| |
Db        365 TCGCTCTACCCCGTTCTGGGCTTCTTCCAGACCCTCAATACGGGCTACTGGAGAGCCCAG 306

Qy        865 GCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAG 924
               ||||||   ||| | || | | |   |  ||| | |  |||   ||   |  ||||
Db        305 TCCAAGACCCCCCTGCCCCTGCTGTTTGCCGACACCTCTGTGCCCGCCAAGGAGCCCAAG 246

Qy        925 CTG 927
              |||
Db        245 CTG 243
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RESULT 13
CNS0071A/c
LOCUS CNS0071A 895 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL066286
VERSION AL066286.1 GI:4945153
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 895)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .895
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14B09"
/clone_lib="RPCI-98"
/note="end : TET3"
ORIGIN

Query Match 3.1%; Score 43.4; DB 10; Length 895;
Best Local Similarity 23.3%; Pred. No. 2.6;
Matches 84; Conservative 114; Mismatches 160; Indels 3; Gaps 1;

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Qy        613 ATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTC 672
              | : ::: |:|: : |::| |: : :|:|    ::  | ::|  |:::  :|:::| | :
Db        808 AMMMMMMCCMCMCMACMMCACMMMAMCMCACAMMMMACMMMAMCAMMMAAMAMMMCMCAM 749

Qy        673 TACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGT 732
               :: :   :: | ||  :| :  |:|| |: | :|    :|   | | | |:|   :|
Db        748 AMMAMAMMMMCCMCCCCMACMMMCMACMCMCCCMCCAMMMCAAMAMAAAAAAMAAAMMAMA 689

Qy        733 CTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTT 792
              |   :: ::||:|:| :  :  | :::::   : ::  ::| |   :|   :    ::
Db        688 CMMMMMMMMCAMCMCMMCCMACACMMMMMMMAMMMMAMMAMCCAMMCACAMMAMCMMCC 629

Qy        793 GACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTAC 852
              | || :|  ||::     :|::     || : |    |     : :|: |  : : : ::
Db        628 MCCCACMMCACCCMMMCMCAMAMM---AMCACMMCAMCACMMMMAMCMCAMMMAMCMAMM 572

Qy        853 AGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATC 912
              : |  |  | :: |||: :  ::::  :|| ::| |:: : :::| ::| :: |:   |
Db        571 MMAAMACACMMMCCAMAMMCMMMMACMCACMMCCAMMAMMMMAMMMCCMMMCMMCMC 512

Qy        913 ACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACC 972
              :||     ::: :   :  |::| | : :|:  |  :|: | | |  ||::    | ||
Db        511 MCCCCCCMMMMMMMAMCCAMMAAAMMCMCMCMCCCMCMACCACCMMCAMMMAACCACCC 452

Qy        973 C 973
              |
Db        451 C 451
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RESULT 14
CL746019
LOCUS CL746019 465 bp DNA linear GSS 27-JUL-2004
DEFINITION OR_BBa0083F15.r OR_BBa Oryza nivara genomic clone OR_BBa0083F15 3',

genomic survey sequence.
ACCESSION CL746019
VERSION CL746019.1 GI:50687811
KEYWORDS GSS.
SOURCE Oryza nivara
ORGANISM Oryza nivara
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 465)
AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR PRimers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
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Plate: 0083 row: F column: 15
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Class: BAC ends.
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/db_xref="taxon:4536"
/clone="OR_BBa0083F15"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Query Match 3.1%; Score 43.2; DB 10; Length 465;
Best Local Similarity 49.0%; Pred. No. 2.5;
Matches 145; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

Qy 751 AACGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTT 810
Db 163 AGCAACCCCATCTGCGAGTCCCAGGTCATCGTCCAGTACCTCGACGACGCCTTCCCCGGC 222

Qy 811 GTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAG 870
Db 223 GGCGCCGCCGGCGGCGACCTCCTCCCCTCCGACCCCCACGCCCGCGCCGTCGCCCGATTC 282

Qy 871 ATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCA 930
Db 283 TGGGCGGCGTACATCGACGCCGAGTTCTTCGCGCCGTGGAACAGGTCGTTCTACACGGCG 342

Qy 931 TACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACC---CTGGGCACAATGGGT 987
Db 343 TCGGAGGAGGAGAAGACGGCGGAGATGGGGAGGGCGGCGGCGGCGCTGGCGACGATCGAG 402

Qy 988 CCAGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACC 1043
Db 403 CGCGCGTTCGCGGAGCTGTCGAGGGGGAAGGGGTTCTTCTCCGGTGAGGACAGGCC 458

RESULT 15
CL736300
LOCUS CL736300 582 bp DNA linear GSS 27-JUL-2004
DEFINITION OR_BBa0070C04.f OR_BBa Oryza nivara genomic clone OR_BBa0070C04 5', genomic survey sequence.
ACCESSION CL736300
VERSION CL736300.1 GI:50670656
KEYWORDS GSS.
SOURCE Oryza nivara
ORGANISM Oryza nivara
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 582)
AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR PRimers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0070 row: C column: 04
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
FEATURES Location/Qualifiers
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/organism="Oryza nivara"
/mol_type="genomic DNA"
/db_xref="taxon:4536"
/clone="OR_BBa0070C04"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Query Match 3.1%; Score 43.2; DB 10; Length 582;
Best Local Similarity 49.0%; Pred. No. 2.7;
Matches 145; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

Qy 751 AACGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTT 810
Db 165 AGCAACCCCATCTGCGAGTCCCAGGTCATCGTCCAGTACCTCGACGACGCCTTCCCCGGC 224

Qy 811 GTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAG 870
Db 225 GGCGCCGCCGGCGGCGACCTCCTCCCCTCCGACCCCCACGCCCGCGCCGTCGCCCGATTC 284

Qy 871 ATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCA 930
Db 285 TGGGCGGCGTACATCGACGCCGAGTTCTTCGCGCCGTGGAACAGGTCGTTCTACACGGCG 344

Qy 931 TACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACC---CTGGGCACAATGGGT 987
Db 345 TCGGAGGAGGAGAAGACGGCGGAGATGGGGAGGGCGGCGGCGGCGCTGGCGACGATCGAG 404

Qy 988 CCAGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACC 1043
Db 405 CGCGCGTTCGCGGAGCTGTCGAGGGGGAAGGGGTTCTTCTCCGGTGAGGACAGGCC 460

Search completed: February 5, 2006, 17:36:33
Job time : 6256 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 13:23:49 ; Search time 937 Seconds
(without alignments)
10050.385 Million cell updates/sec

Title: US-10-733-031-5
Perfect score: 1413
Sequence: 1 aacaccaacaaggcaaccgc.....tggcagcaccactcatcgga 1413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1413	100.0	1413	12	ADP86102	Adp86102 Infectiou
	2	1413	100.0	1485	12	ADP86103	Adp86103 Barely al
	3	1390.6	98.4	3097	2	AAZ25385	Aaz25385 Infectiou
	4	1390.6	98.4	3097	8	ABZ58597	Abz58597 Infectiou
	5	1342.6	95.0	1554	2	AAV12202	Aav12202 Infectiou
	6	1043.4	73.8	2950	4	AAH45585	Aah45585 Birnaviru
	7	994.4	70.4	3097	2	AAZ25383	Aaz25383 Infectiou
	8	951	67.3	1362	12	ADP20604	Adp20604 Infectiou
	9	753	53.3	780	3	AAZ50081	Aaz50081 Infectiou
	10	262.6	18.6	3264	2	AAV26606	Aav26606 Plasmid p
	11	246	17.4	3260	4	AAF25059	Aaf25059 Nucleotid
	12	240.6	17.0	1471	2	AAT63072	Aat63072 DNA seque
	13	238.8	16.9	3180	2	AAQ45441	Aaq45441 Sequence
	14	238.8	16.9	3230	2	AAT05623	Aat05623 IBDV GLS
	15	237.4	16.8	1471	2	AAQ14896	Aaq14896 E/DEL-2 c
	16	237.2	16.8	3180	2	AAT05624	Aat05624 IBDV E/DE
	17	237.2	16.8	3228	2	AAQ14897	Aaq14897 GLS clone
	18	235.6	16.7	3230	2	AAT63065	Aat63065 DNA seque
	19	235.6	16.7	7595	14	AEB46344	Aeb46344 Plasmid p
	20	235.6	16.7	7595	14	AEB54480	Aeb54480 Plasmid D
c	21	235.6	16.7	9600	14	AEB46348	Aeb46348 Plasmid p
c	22	235.6	16.7	9600	14	AEB54486	Aeb54486 Plasmid D
c	23	235.6	16.7	10909	13	ADT08325	Adt08325 Novel IBD
	24	234	16.6	3261	2	AAV26605	Aav26605 Plasmid p
	25	234	16.6	3261	2	AAV99789	Aav99789 cDNA sequ
	26	234	16.6	3261	2	AAV99790	Aav99790 cDNA sequ
	27	234	16.6	3261	2	AAX36388	Aax36388 IBDV cons
	28	234	16.6	3261	6	ABK13128	Abk13128 DNA encod
	29	233.8	16.5	3004	10	ADH71087	Adh71087 Infectiou
	30	233.8	16.5	3004	10	ADH62843	Adh62843 Infectiou
	31	232.8	16.5	3269	3	AAZ51840	Aaz51840 DNA encod
	32	232.4	16.4	3039	13	ADW00503	Adw00503 Polymer p
	33	232.4	16.4	3257	2	AAT31897	Aat31897 IBDV larg
	34	232.4	16.4	3260	4	AAF25060	Aaf25060 Nucleotid
	35	232	16.4	3260	4	AAF25061	Aaf25061 Nucleotid
	36	231.2	16.4	3060	2	AAQ63680	Aaq63680 Segment A
	37	231.2	16.4	3115	2	AAQ31857	Aaq31857 IBDV stra
	38	231.2	16.4	3129	1	AAN60874	Aan60874 Large RNA
	39	230.8	16.3	3180	2	AAQ45247	Aaq45247 Sequence
	40	228.6	16.2	2391	2	AAT43284	Aat43284 Coding se
	41	226	16.0	1428	4	AAI64576	Aai64576 IBDV stru
	42	224.4	15.9	3148	5	AAH41061	Aah41061 Infectiou
	43	223.4	15.8	1374	10	ACC69333	Acc69333 IBDV E st
	44	222.8	15.8	3257	2	AAQ42757	Aaq42757 IBDV gene
	45	221.6	15.7	3087	2	AAQ46181	Aaq46181 IBDV stru

ALIGNMENTS

RESULT 1
ADP86102
ID ADP86102 standard; DNA; 1413 BP.
XX
AC ADP86102;
XX
DT 23-SEP-2004 (first entry)
XX
DE Infectious pancreatic necrosis virus (IPNV) VP2 DNA.
XX
KW Transgenic plant; immunostimulant; vaccine; therapy;
KW immunogenic response; VP2 protein; IPNV;
KW Infectious pancreatic necrosis virus; gene; ds.
XX
OS Infectious pancreatic necrosis virus.
XX
PN WO2004055190-A2.
XX
PD 01-JUL-2004.
XX
PF 12-DEC-2003; 2003WO-EP014137.
XX
PR 13-DEC-2002; 2002US-0433381P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (PROD-) PRODIGENE INC.
XX
PI Beifuss K, Bootland LM;
XX
DR WPI; 2004-488070/46.
XX
PT New transgenic plant or transgenic plant material producing a peptide or
PT polypeptide useful for generating an antigenic or immunogenic response in
PT fish.
XX
PS Claim 8; SEQ ID NO 5; 48pp; English.
XX
CC The present invention relates to a transgenic plant or transgenic plant
CC material engineered to express a nucleotide sequence encoding an amino
CC acid sequence that produces an antigenic or immunogenic response when
CC administered to a fish. The invention act as a immunostimulant. The

CC invention is useful for preparing vaccine, manufacturing medicament for
CC therapeutic or prophylactic treatment of fish and for generating an
CC antigenic or immunogenic response in the fish e.g. salmonid fish. The
CC present sequence is a infectious pancreatic necrosis virus (IPNV) VP2
CC protein encoding DNA. This sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 1413 BP; 404 A; 426 C; 348 G; 235 T; 0 U; 0 Other;

Query Match 100.0%; Score 1413; DB 12; Length 1413;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
              |||||||||||||||||||||||||||||||
Db       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
```

RESULT 2
ADP86103
ID ADP86103 standard; DNA; 1485 BP.
XX
AC ADP86103;
XX
DT 23-SEP-2004 (first entry)
XX
DE Barely alpha amylase secretion signal - IPNV VP2 chimaeric DNA.
XX
KW Transgenic plant; immunostimulant; vaccine; therapy;
KW immunogenic response; VP2 protein; barely; BAASS;
KW barely alpha amylase secretion signal; IPNV;
KW Infectious pancreatic necrosis virus; chimaeric; gene; ds.
XX
OS Infectious pancreatic necrosis virus.
OS Zea mays.
OS Chimeric.
XX
PN WO2004055190-A2.
XX
PD 01-JUL-2004.
XX
PF 12-DEC-2003; 2003WO-EP014137.
XX
PR 13-DEC-2002; 2002US-0433381P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (PROD-) PRODIGENE INC.
XX
PI Beifuss K, Bootland LM;
XX
DR WPI; 2004-488070/46.
XX
PT New transgenic plant or transgenic plant material producing a peptide or

```
PT   polypeptide useful for generating an antigenic or immunogenic response in
PT   fish.
XX
PS   Claim 8; SEQ ID NO 6; 48pp; English.
XX
CC   The present invention relates to a transgenic plant or transgenic plant
CC   material engineered to express a nucleotide sequence encoding an amino
CC   acid sequence that produces an antigenic or immunogenic response when
CC   administered to a fish. The plant-expressed recombinant protein act as a
CC   immunostimulant. The invention is useful for preparing vaccine,
CC   manufacturing medicament for therapeutic or prophylactic treatment of
CC   fish and for generating an antigenic or immunogenic response in the fish
CC   e.g. salmonid fish. The present sequence is a barely alpha amylase signal
CC   sequence (BAASS) - infectious pancreatic necrosis virus (IPNV) VP2
CC   chimaeric DNA. This sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 1485 BP; 412 A; 458 C; 364 G; 251 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1413;  DB 12;  Length 1485;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1413;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 132

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 192

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 252

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 312

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 372

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 432

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 492

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 552

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 612

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 672

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 732

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 792

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        793 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 852

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 912

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 972

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1032

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1092

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1152

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1212

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1272

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1332

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1392

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1452

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
              |||||||||||||||||||||||||||||||
Db       1453 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1485


RESULT 3
AAZ25385
ID   AAZ25385 standard; cDNA; 3097 BP.
XX
AC   AAZ25385;
XX
DT   16-DEC-1999  (first entry)
XX
DE   Infectious pancreatic necrosis virus strain SP segment A clone.
XX
KW   Infectious pancreatic necrosis virus; IPNV; strain West Buxton;
KW   strain SP; segment A; segment B; nonpathogenic; Birnavirdae family;
KW   infection; live attenuated vaccine; aquaculture industry; Rainbow trout;
KW   Brook trout; Atlantic salmon; ss.
XX
OS   Infectious pancreatic necrosis virus.
XX
PN   WO9950419-A2.
XX
PD   07-OCT-1999.
XX
PF   31-MAR-1999;   99WO-US004285.
XX
PR   31-MAR-1998;   98US-0080178P.
XX
PA   (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
```

XX
PI Vakharia VN, Yao K;
XX
DR WPI; 1999-591321/50.
XX
PT Preparing nonpathogenic infectious pancreatic necrosis virus, IPNV,
PT useful for producing attenuated virus for vaccines useful in the
PT aquaculture industry.
XX
PS Disclosure; Page 41-42; 63pp; English.
XX
CC A method has been developed for preparing nonpathogenic, infectious
CC pancreatic necrosis virus (IPNV). The method comprises: 1) preparing cDNA
CC containing the IPNV genome segments A and B where A is modified to
CC prevent expression of an arginine-rich non-structural (NS) protein; 2)
CC transcribing the cDNA to produce RNA; 3) incubating the host cells in a
CC culture medium; and 4) isolating live IPNV from the culture medium. The
CC method is useful to produce live nonpathogenic IPNV, useful to study
CC viral pathogenesis and for the production of live, nonpathogenic IPNV
CC vaccines, since it was demonstrated that the NS protein-deficient virus
CC could replicate but did not invoke a pathological response in hosts.
CC Combination vaccines may also be produced by combining the IPNV with
CC bacterial antigens (especially from gram negative bacteria e.g. Aeromonas
CC salmonicida) and/or antigens from aquatic viruses other than Birnaviruses
CC (the family to which IPNV belongs) e.g. infectious haematopoietic
CC necrosis virus. The method may also be used to generate a nonpathogenic
CC chimeric virus when the cDNA of segment A encodes epitopic determinants
CC from at least two different IPNV strains. IPNV causes a highly contagious
CC and destructive disease of juvenile Rainbow and Brook trout and Atlantic
CC salmon (e.g. highly virulent strains can cause more than 90 % mortality
CC in hatchery stocks less than 4 months old and survivors can remain
CC lifelong carriers and reservoirs of infection); IPNV is therefore a
CC pathogen of major economic importance to the aquaculture industry. The
CC present sequence represents IPNV strain SP segment A cDNA
XX
SQ Sequence 3097 BP; 890 A; 932 C; 797 G; 478 T; 0 U; 0 Other;

Query Match 98.4%; Score 1390.6; DB 2; Length 3097;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        122 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        182 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACAAGAGACCTCGTCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AACTTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 301

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGTTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        482 AACGCTGCCACCTTCGAGGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAGCCATACGTCCGCCTAGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGGGCC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        782 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACGACAGTGACGGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        842 ATAAACTTCAGTCTGGCAGAACAACCCGCAGTCGAGACCAAGTTCGACTTCCAGCTGGAC 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTCGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1441

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
              ||||||||||||||||||||||||||||| |||
Db       1502 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1534
```

RESULT 4
ABZ58597
ID ABZ58597 standard; cDNA; 3097 BP.
XX
AC ABZ58597;
XX
DT 13-MAY-2003 (first entry)
XX

DE Infectious pancreatic necrosis virus Segment A cDNA.
XX
KW IPNV; vaccine; gene; ss.
XX
OS Infectious pancreatic necrosis virus.
XX
FH Key Location/Qualifiers
FT CDS 119. .3037
FT /*tag= a
FT /product= "VP2-VP4-VP3"
XX
PN WO2003013597-A1.
XX
PD 20-FEB-2003.
XX
PF 12-AUG-2002; 2002WO-US025185.
XX
PR 10-AUG-2001; 2001US-0311488P.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Vakharia VN;
XX
DR WPI; 2003-256495/25.
DR P-PSDB; ABP72396.
XX
PT New sub-unit vaccine comprising IPNV structural proteins VP2 and VP3
PT assembled as an empty IPNV capsid, useful for controlling Infectious
PT Pancreatic Necrosis Virus (IPNV) in aquatic species.
XX
PS Claim 10; Page 34-36; 46pp; English.
XX
CC The present sequence is a full-length cDNA encoding Segment A (V2-V4-V3)
CC of a Norwegian field isolate (Sp serotype (ALV122)) of infectious
CC pancreatic necrosis virus (IPNV), the causal agent of a highly contagious
CC and destructive disease of juvenile Rainbow and Brook trout and Atlantic
CC salmon. VP2 and VP3 are IPNV structural proteins whereas VP4 is a non-
CC structural protein. The present sequence was generated by RT-PCR using
CC the primers given in ABZ58598-600 and ABZ70365, and using genomic RNA as
CC template. A claimed subunit vaccine for controlling IPNV in aquatic
CC species comprises IPNV VP2 and VP3 assembled as an empty capsid, and
CC optionally also comprises a green fluorescent protein (GFP). A claimed
CC baculovirus vector comprises a polynucleotide sequence encoding for VP2-
CC VP4-VP3 of IPNV, especially the present sequence, and a GFP (see
CC ABZ58594). A claimed method of generating structural proteins of IPNV
CC assembled as an empty viral capsid involves: providing a recombinant
CC baculovirus comprising a polynucleotide encoding IPNV segment A proteins
CC VP2-VP4-VP3 and a reporter protein; infecting insect larvae with the
CC recombinant baculovirus; maintaining suitable conditions for expression
CC of the IPNV proteins VP2-VP4-VP3 and the reporter protein to generate
CC structural proteins VP2 and VP3 assembled as an empty IPNV capsid; and
CC recovering the empty IPNV capsid from the larvae
XX
SQ Sequence 3097 BP; 898 A; 930 C; 793 G; 476 T; 0 U; 0 Other;

Query Match 98.4%; Score 1390.6; DB 8; Length 3097;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||| |||||||||||||||||| |||||||||| ||||||||||||||||||||||||
Db        122 AACACAAACAAGGCAACCGCAACTTACCTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        182 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACAAGAGACCTCGTCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AACTTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 301

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AAATATGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAACTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTACTGCGACAGGAACC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        782 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACGACAGTGACGGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              ||||||||||||||| |||||||||||||  ||||||||||||||||||||||||||||
Db        842 ATAAACTTCAGTCTGACAGAACAACCCGCAGTCGAGACCAAGTTCGACTTCCAGCTGGAC 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTA 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1441
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Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
             |||||||||||||||||||||||||||| |||
Db       1502 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1534


RESULT 5
AAV12202
ID   AAV12202 standard; DNA; 1554 BP.
XX
AC   AAV12202;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Infectious pancreatic necrosis virus VP2 gene.
XX
KW   Infectious pancreatic necrosis virus; IPNV; VP2; vaccine; fish;
KW   immunisation; VR-299; SP serotype; viral A segment; ss.
XX
OS   Infectious pancreatic necrosis virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             37. .1554
FT                   /*tag= a
FT                   /product= "VP2"
FT                   /note= "no stop codon given"
XX
PN   US5165925-A.
XX
PD   24-NOV-1992.
XX
PF   02-MAY-1989;   89US-00346623.
XX
PR   02-MAY-1989;   89US-00346623.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Leong JC;
XX
DR   WPI; 1992-414903/50.
DR   P-PSDB; AAW44158.
XX
PT   Vaccine for infectious pancreatic necrosis virus in fish - comprises
PT   polypeptide from viral A segment including VP2, produced by bacterial
PT   expression.
XX
PS   Claim 1; Fig 15; 28pp; English.
XX
CC   The present sequence encodes the VP2 protein from infectious pancreatic
CC   necrosis virus (IPNV). A vaccine has been developed for immunising
CC   susceptible fish against infection by VR-299 or SP serotypes of the IPNV.
CC   The vaccine comprises an IPNV polypeptide from the viral A segment and
CC   includes at least VP2. The vaccine is capable of inducing immunity in the
CC   fish to subsequent infection by the VR-299 or SP serotypes of IPNV. The
CC   polypeptide is produced by an expression vector in a compatible bacterial
CC   host, where the vector includes an inserted DNA sequence from the A
CC   segment of the viral DNA coding for the IPNV polypeptide in the vaccine.
CC   Large amounts of the IPNV polypeptide can be produced by the transformed
CC   bacteria. The bacterial lysate containing the viral protein can be added
CC   directly to water containing the fish to simultaneously immunise large
CC   numbers of fish, particularly young fish
XX
SQ   Sequence 1554 BP; 445 A; 451 C; 398 G; 260 T; 0 U; 0 Other;

  Query Match             95.0%;  Score 1342.6;  DB 2;  Length 1554;
  Best Local Similarity   96.9%;  Pred. No. 0;
  Matches 1369;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              |||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         40 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 99

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              |||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||
Db        100 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACCAGAGACCTCGTCATAC 159

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        160 AACTTAGAGGTCCCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 219

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TCACGGATCGGCGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 279

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||  |   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 TGCTGGAGAGCGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 339

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        340 AAATACGACATTCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 399

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              |||||||||||||| ||||||||||||||||||||||||||||||||| ||||||||||
Db        400 AACGCTGCCACCTTTGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAATAGCCTG 459

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        460 ATGTCCCTAACTACGAACCCCCAGGACAAAGCCAACAACCAGCTGGTGACCAAAGGAGTC 519

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 ACCGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 579

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        580 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAGGATGAGGTGCACAGCTGCAATTGCACCA 639

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        640 CGGAGGTACGAGATCGACCTCCCATCCCAAAGCCTACCCCCCGTTCCTGCGACAGGAACC 699

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 CTGACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 759

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        760 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAGGTTCGACTTCCAGCTGGAC 819

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              || |||||||||||| |||||||||| ||||||||||||||||||||||||||||||||
Db        820 TTGATGGGCCTTGACAATGACGTCCCAGTGGTCACAGTGGTCAGCTCCGTGCTGGCCACA 879

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 AACGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATT 939

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 ACCAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 999

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              || |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||||
Db       1000 AATGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTTTCATCGGGGAACGGA 1059

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1060 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCATATGAGAAGATGACACCGCTG 1119

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1120 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1179

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1239

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1299

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              |||||||||||||||||||||||||||||  ||     |||||||||||||||||||||||
Db       1300 GAGAGGACCAGAGTCTTCAACGAAATCACAGAGAAGACCAGTGACCTGCCCACGTCAAAG 1359

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
              |||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||
Db       1360 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGAAAAATCGCAGCTCCTGTACTGTCC 1419

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
              |||||||||||||||||||||||||||||| |||
Db       1420 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1452


RESULT 6
AAH45585
ID   AAH45585 standard; cDNA; 2950 BP.
XX
AC   AAH45585;
XX
DT   13-SEP-2001  (first entry)
XX
DE   Birnavirus structural gene segment A cDNA.
XX
KW   Birnaviral antigen; segment A; structural gene; ss.
XX
OS   Yellowtail ascites virus.
XX
PN   JP2001097884-A.
XX
PD   10-APR-2001.
XX
PF   29-SEP-1999;   99JP-00276430.
XX
PR   29-SEP-1999;   99JP-00276430.
XX
PA   (HARA/) HARA S.
PA   (NORQ ) NORINSUISANSHO YOSHOKU KENKYU.
XX
DR   WPI; 2001-360547/38.
XX
PT   Visnavirus antigen substance comprising the cDNA fragment of visnavirus
PT   structural gene segment A recombined to a baculovirus vector is useful
PT   for prevention and diagnosis of infection.
XX
PS   Claim 2; Page 7-8; 8pp; Japanese.
XX
CC   This invention relates to a Birnaviral antigen containing substance,
CC   which comprises cDNA encoding segment A of a birnavirus structural gene
CC   recombined with a baculoviral vector. The birnaviral antigen substance
CC   can be used for preventing birnavirus infection and also as a diagnostic
CC   material for the detection of birnavirus infection. The present sequence
CC   represents the cDNA sequence of segment A of Yellowtail ascites virus
CC   (Birnavirus) structural gene used in the invention
XX
SQ   Sequence 2950 BP; 867 A; 870 C; 739 G; 474 T; 0 U; 0 Other;

  Query Match             73.8%;  Score 1043.4;  DB 4;  Length 2950;
  Best Local Similarity   83.7%;  Pred. No. 1.2e-282;
  Matches 1182;  Conservative    0;  Mismatches  231;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              |||||  |  ||||||||||||||||||||||| |||||| |||||||| |||| ||| |||
Db          4 AACACAACAAAGGCAACCGCAACTTACTTGAGATCCATTATGCTTCCCGAGAATGGTCCA 63

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              ||||||||  |||||||||||||| |||||||||| ||||||||||||||||||||||||
Db         64 GCAAGCATTCCGGACGACATAACAGAGAGACACATACTAAAACAAGAGACCTCGTCATAC 123

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              |||  ||||||||||  ||  ||  ||||||||  |||||||  ||  ||||||||  ||  ||
Db        124 AACTTAGAGGTCTCAGACTCCGGAAGTGGGCTTCTTGTCTGCTTCCCTGGAGCTCCTGGA 183

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||   |  |||||||  |||||||  ||||||||||||||||||  |||  |||  |||||||||
Db        184 TCCAGAGTCGGTGCCCACTACAAGTGGAATGCGAACCAGACCAGGCAGGAATTCGACCAG 243

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||||||  |  ||  ||  ||||||||||||||  ||  ||||||||||||||||||||||  ||
Db        244 TGGCTGAAAACATCACAGGACCTGAAGAAGGCATTCAACTACGGGAGGCTGATCTCACGG 303

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              |||||||||  ||||  |||||  ||  |||||  ||  |||||  |||||  |||||  ||
Db        304 AAATACGACGTCCAGAGCTCAACCCTACCTGCTGGTCTGTATGCCCTGAATGGGACCCTG 363

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              |||||  ||  ||||||||||| ||||||||||  |||||||||  |  ||||||||||  |||
Db        364 AACGCCGCGACCTTCGAAGGAAGTCTGTCTGAAGTGGAGAGCTTCTCCTACAACAGTCTG 423

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||  ||  ||||||||||||||||||||  |||||||||  ||  ||||||||||
Db        424 ATGTCCCTCACCACGAACCCCCAGGACAAAGTGAACAACCAGCCAGTCACCAAAGGAGTG 483

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              ||||||||  ||  ||||||||||||||||||||  ||||||||||||  ||||||||||
Db        484 ACAGTCCTAAACCTACCAACAGGGTTCGACAAGCCATACGTCCGCCTGGAGGACGAGACC 543

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||  ||  ||  |  ||||||||||||||||  |||  |||||||||||||||||||||||||
Db        544 CCACAAGGGCCCCAGTCAATGAACGGCGCCCGGATGAGGTGCACAGCTGCAATTGCACCA 603

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              ||  ||||||||  ||||||||||||||||  ||||||  |||  |  ||  ||  |||||  ||  |||
Db        604 CGAAGGTACGAAATCGACCTCCCATCCGCACGCCTCCCCACAGTACCAGCGACTGGGACC 663

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              |||||  ||  |  ||  ||  ||||||||||||  ||  ||||  ||  ||||||||  ||  |||
Db        664 CTCACAACAATGTATGAAGGGAACGCCGACATTGTGAACTCAACCACAGTGACCGGCGAC 723

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              ||  |  ||||||  ||||    ||  |  |||  |  |||||  ||  ||||  ||||||||||||  |||
Db        724 ATCAGCTTCAGACTGGATCAAGACCCCCCGAACGACACGAAGTACGACTTCCAGCTCGAC 783

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              |||  |  |||  |  ||||||  |||||||  ||  ||  ||  |  |||||    ||||||||||
Db        784 TTCCTCGGCTTAGACAACAACGTCCCCGTCGTGTCAATAACCAGCTATACGCTGGCCACA 843

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              |  ||||||||||  ||  |||||||  |||  |  ||  |||||  |||||  ||  ||||  |||
Db        844 ACCGACAACTACAGGGGGGTCTCAGTCAAATTCACACAGTCAATCCCAACAGAGACAATC 903

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              |||||  ||  |||||||||||||||||||  |||||  ||||||||||||||||||  ||||||
Db        904 ACAAAACCCATCACCAGGGTCAAGCTGTCCTACAAAATCAACCAGCAGACAGCCATCGGC 963

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||  |  ||  ||  ||  ||  |  ||||  ||  ||||||||||  ||||||||||  |||||
Db        964 AATGCAGCAACGCTTGGACCCCTGGGGCCCTCATCCGTCTCATTCTCATCAGGAAACGGC 1023

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||  ||  ||  ||  ||||||||  ||||||||  ||  ||||||||||||  ||  |  |
Db       1024 AACGTACCTGGAGTGCTCAGGCCAATCACCCTGGTGGCGTACGAGAAGATGACCCCCCAG 1083

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||  ||||||||  |||||||||||||| |||||||||||||||||||||||  ||||||||
Db       1084 TCGATCCTGACGGTAGCTGGAGTGTCAAACTACGAGCTGATCCCAAACCCCGAACTCCTG 1143
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Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              |||||||||| ||    |||||||||| ||||| |||||||||||||| |||||||||
Db       1144 AAGAACATGGTCACGAAATATGGCAAGTATGACCCTGAAGGTCTCAACTACGCCAAGATG 1203

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              |||||||||||| | || ||||| |||||||| ||||| ||||| || ||||||||||||
Db       1204 ATCCTGTCCCACCGAGAGGAGCTAGACATCAGAACAGTCTGGAGAACCGAGGAGTACAAG 1263

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||| || |||| |||||| || ||||| |||||||| |||||||| || || |||||
Db       1264 GAGAGAACAAGAGCCTTCAATGAGATCACAGACTTCTCAAGTGACCTCCCAACCTCAAAA 1323

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
              || ||||| |||||||||| || ||||| || ||||| || ||||| || ||  ||||
Db       1324 GCCTGGGGGTGGAGAGACATTGTGAGAGGCATCCGGAAGGTGGCAGCACCAGTGTTGTCA 1383

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
              || || || || ||||| ||||||||||||||
Db       1384 ACACTCTTCCCCATGGCGGCACCACTCATCGGA 1416
```

RESULT 7
AAZ25383
ID AAZ25383 standard; cDNA; 3097 BP.
XX
AC AAZ25383;
XX
DT 16-DEC-1999 (first entry)
XX
DE Infectious pancreatic necrosis virus strain West Buxton segment A clone.
XX
KW Infectious pancreatic necrosis virus; IPNV; strain West Buxton;
KW strain SP; segment A; segment B; nonpathogenic; Birnavirdae family;
KW infection; live attenuated vaccine; aquaculture industry; Rainbow trout;
KW Brook trout; Atlantic salmon; ss.
XX
OS Infectious pancreatic necrosis virus.
XX
PN WO9950419-A2.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US004285.
XX
PR 31-MAR-1998; 98US-0080178P.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Vakharia VN, Yao K;
XX
DR WPI; 1999-591321/50.
XX
PT Preparing nonpathogenic infectious pancreatic necrosis virus, IPNV,
PT useful for producing attenuated virus for vaccines useful in the
PT aquaculture industry.
XX
PS Disclosure; Page 37-38; 63pp; English.
XX
CC A method has been developed for preparing nonpathogenic, infectious
CC pancreatic necrosis virus (IPNV). The method comprises: 1) preparing cDNA
CC containing the IPNV genome segments A and B where A is modified to
CC prevent expression of an arginine-rich non-structural (NS) protein; 2)
CC transcribing the cDNA to produce RNA; 3) incubating the host cells in a
CC culture medium; and 4) isolating live IPNV from the culture medium. The
CC method is useful to produce live nonpathogenic IPNV, useful to study
CC viral pathogenesis and for the production of live, nonpathogenic IPNV
CC vaccines, since it was demonstrated that the NS protein-deficient virus
CC could replicate but did not invoke a pathological response in hosts.
CC Combination vaccines may also be produced by combining the IPNV with
CC bacterial antigens (especially from gram negative bacteria e.g. Aeromonas
CC salmonicida) and/or antigens from aquatic viruses other than Birnaviruses
CC (the family to which IPNV belongs) e.g. infectious haematopoietic
CC necrosis virus. The method may also be used to generate a nonpathogenic
CC chimeric virus when the cDNA of segment A encodes epitopic determinants
CC from at least two different IPNV strains. IPNV causes a highly contagious
CC and destructive disease of juvenile Rainbow and Brook trout and Atlantic
CC salmon (e.g. highly virulent strains can cause more than 90 % mortality
CC in hatchery stocks less than 4 months old and survivors can remain
CC lifelong carriers and reservoirs of infection); IPNV is therefore a
CC pathogen of major economic importance to the aquaculture industry. The
CC present sequence represents IPNV strain West Buxton segment A cDNA
XX
SQ Sequence 3097 BP; 885 A; 891 C; 795 G; 526 T; 0 U; 0 Other;

Query Match 70.4%; Score 994.4; DB 2; Length 3097;
Best Local Similarity 81.5%; Pred. No. 7.4e-269;
Matches 1151; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

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Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              |||||  |  ||||||||||||||||||||||| |||||| |||||||| |||| |||||||
Db        122 AACACAACAAAGGCAACCGCAACTTACTTGAGATCCATTATGCTTCCCGAGAATGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              |||||||| |||||||||||||| |||||||||| |||||||||||||||| ||||||
Db        182 GCAAGCATTCCGGACGACATAACAGAGAGACACATACTAAAACAAGAGACCTCATCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||| |||||||||||| |||||||||| ||||||| || |||||||||| || ||
Db        242 AACTTAGAGGTCTCCGACTCAGGAAGTGGGCTTCTTGTCTGCTTCCCTGGGGCTCCCGGA 301

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||  |  ||||||| |||||||| |||||  |||||||||||  ||||| |||||||||
Db        302 TCCAGAGTCGGTGCCCACTACAGGTGGAATCTGAACCAGACGGAACTGGAATTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||| |||| || || |||||||||||||||| |||||||||||||| |||||||| ||
Db        362 TGGTTGGAAACATCACAGGACCTGAAGAAAGCATTCAACTACGGGAGGTTGATCTCACGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              |||||||||||||| ||||| || || || || || |||||||| || |||||||| ||
Db        422 AAATACGACATCCAGAGCTCGACCCTTCCCGCTGGCCTCTATGCACTCAACGGGACCCTG 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              || || || |||||||||| ||||| ||||||||||||||||||||||||| |||||| ||
Db        482 AATGCAGCTACCTTCGAAGGAAGTCTTTCTGAGGTGGAGAGCCTGACCTATAACAGCTTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              |||||||| ||||| ||||| |||||||| |||||||||| || |||||||||||| |
Db        542 ATGTCCCTGACAACAAACCCTCAGGACAAGGTCAACAACCAACTAGTGACCAAAGGAATA 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              || |||||||| || ||||| ||||| ||||| |||||||||||||| ||||||||||||
Db        602 ACCGTCCTGAACCTTCCAACTGGGTTTGACAAGCCATACGTCCGCCTTGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              || ||||| | |||||| |||||||| |||| |||||||||||| |||||||| |||||
Db        662 CCGCAGGGCCCCCAGTCCATGAACGGAGCCAGGATGAGGTGCACCGCTGCAATCGCACCA 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
               |||||||||| || |||||||||||  | ||||||||  ||||  | || || || |||
Db        722 AGGAGGTACGAAATAGACCTCCCATCTGAGCGCCTACCAACCGTGGCAGCAACTGGGACC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              |  || ||  |||| || || |||||||||| || ||||| || |||||||| ||||||
Db        782 CCAACAACAATCTATGAAGGGAACGCCGACATTGTGAACTCAACCACAGTGACAGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              ||| ||||   || ||||  ||||||  ||||||||   ||||||||||   ||  |
Db        842 GTAACCTTCCAACTAGCAGCCGAACCCGTCAACGAGACGCGGTTCGACTTCATCCTACAA 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              ||| | || |||||||| || || || || ||| | |||   |||||    |||| |||
Db        902 TTCCTTGGGCTTGACAATGATGTGCCCGTGGTCTCCGTGACAAGCTCAACCCTGGTCACG 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
                 |||||||||||| || | ||| |||||| | || ||||| ||||| || ||    ||
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Db        962 GCCGACAACTACAGGGGTGCCTCCGCCAAGTTTACGCAGTCAATCCCAACGGAACTAATA 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960

Db       1022 ACTAAGCCCATTACAAGGGTCAAGCTGGCTTACCAGCTCAACCAGCAGACCGCAATCGGA 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020

Db       1082 AACGCCGCAACACTCGGGGCCAAAGGACCCCCGTCAGTCTCATTCTCATCAGGGAATGGC 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080

Db       1142 AATGTGCCGGGGGTTCTAAGACCCATAACCTTGGTGGCATACGAAAAGATGACCCCCCAG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140

Db       1202 TCAATTCTGACCGTGGCCGGCGTATCCAACTATGAGCTGATCCCCAACCCAGACCTCCTG 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200

Db       1262 AAGAACATGGTCACCAAGTATGGCAAATATGACCCTGAGGGCCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260

Db       1322 ATCCTGTCCCACAGGGAGGAGCTAGACATTAGAACTGTCTGGAGGACCGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320

Db       1382 GAGAGGACAAGAGCCTTCAATGAGATCACTGACTTCACAAGTGACCTGCCAACATCAAAA 1441

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380

Db       1442 GCATGGGGGTGGAGAGACCTGGTCAGAGGCATCAGAAAAGTGGCAGCACCAGTGCTGTCA 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGG 1412

Db       1502 ACGCTCTTCCCAATGGCCGCCCCACTTATAGG 1533
```

```
RESULT 8
ADP20604
ID   ADP20604 standard; DNA; 1362 BP.
XX
AC   ADP20604;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Infectious pancreatic necrosis virus (IPNV) VP2 gene sequence SeqID23.
XX
KW   infectious pancreatic necrosis virus; IPNV; VP2; vaccine; fish; VP3;
KW   gene; ds.
XX
OS   Infectious pancreatic necrosis virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1362
FT                   /*tag=  a
FT                   /product= "Infectious pancreatic necrosis virus (IPNV)
FT                   VP2 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   KR2003078806-A.
XX
PD   08-OCT-2003.
XX
PF   31-MAR-2003; 2003KR-00020240.
XX
PR   30-MAR-2002; 2002KR-00017669.
XX
PA   (RNAR-) RNA INC.
XX
PI   Jung DG,  Park JU,  Kim HG,  Lee JM,  Mun CH,  Kim JS;
XX
DR   WPI; 2004-164334/16.
DR   P-PSDB; ADP20605.
XX
PT   Vaccine composition for treatment and prevention of infectious pancreatic
PT   necrosis viruses comprises VP2 or VP3 gene.
XX
PS   Example 1; SEQ ID NO 23; 1pp; Korean.
XX
CC   This invention relates to an infectious pancreatic necrosis viruses
CC   (IPNV) VP2 structure protein and eukaryote expression vector containing
CC   the encoding gene. A vaccine composition for the treatment and prevention
CC   of infectious pancreatic necrosis viruses (IPNV) in fish comprises the
CC   expression vectors containing the gene of infectious pancreatic necrosis
CC   viruses (IPNV) VP2 gene or VP3 gene or both genes. The present sequence
CC   is that of the gene which encodes the Infectious pancreatic necrosis
CC   viruses (IPNV) VP2 protein of the invention.
XX
SQ   Sequence 1362 BP; 406 A; 391 C; 335 G; 230 T; 0 U; 0 Other;
```

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  Query Match            67.3%;  Score 951;  DB 12;  Length 1362;
  Best Local Similarity  81.2%;  Pred. No. 8.6e-257;
  Matches 1104;  Conservative    0;  Mismatches  255;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60

Db          4 AGCACAACCAAGGCAACCGCAACCTACTTGAGATCCATTATGCTTCCCGAGAATGGGCCA 63

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120

Db         64 GCAAGCATTCCGGACGACATAACAGAGAGGCATATACTAAAACAAGAGACCTCGTCATAC 123

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180

Db        124 AACTTAGAGGCATCCGAATCAGGAAGTGGGCTTCTTGTCTGCTTCCCCGGAGCTCCTGGA 183

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240

Db        184 TCCAGGGTCGGTGCCCACTACAGGTGGAATCTGAACCAGACGGCACTAGAATTCGACCAG 243

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300

Db        244 TGGCTAGAGACGTCACAGGACCTAAAGAAGGCATTCAACTACGGGAGACTGATCTCACGG 303

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360

Db        304 AAATACCACATCCAGAGCTCAACCCTTCCCGCTGGTCTGTATGCACTCAATGGGACCCTG 363

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420

Db        364 AACGCTGCCACCTTCGAAGGAAGTCTGTCTGAAGTAGAGAGCCTAACCTACAACAGCTTG 423

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480

Db        424 ATGTCCCTAACAACAAACCCACAGGACAAGGTCAACAATCAACTAGTGACCAAAGGAATT 483

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540

Db        484 ACCGTCCTGAATCTACCAACTGGGTTTGACAAGCCATACGTCCGCCTAGAGGACGAGACA 543

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600

Db        544 CCACAGGGCCCCCAGTCCATGAACGGAGCAAGGATGAGGTGCACAGCTGCCATCGCACCA 603

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660

Db        604 AGGAGGTATGAAATCGACCTCCCATCCGAACGACTGCCGACCGTGGCCGCGACTGGGACC 663

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720

Db        664 CCAACAACAATTTATGAGGGGAATGCTGACATCGTGAACTCCACAGCAGTCACCGGGGAC 723

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Db        724 ATAACATTCCAGCTCGAGGCCGAACCCGTCAATGAGACACGGTTCGACTTCATTCTACAG 783

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840

Db        784 TTCCTGGGGCTGGACAACGACGTCCCCGTGGTTACCGTGACAAGCTCCACGCTAGTCACA 843

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900

Db        844 GCGGACAACTACAGGGGGGCGTCAGCCAAGTTCACCCAGTCAATCCCAACAGAAATGATT 903

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960

Db        904 ACCAAACCAATCACACGGGTCAAGCTGGCCTACCAGCTCAACCGGCAGACCGCAATTGCA 963

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020

Db        964 AACGCAGCAACGCTCGGAGCCAAGGGGCCGGCATCAGTCTCATTCTCATCCGGGAACGGC 1023

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080

Db       1024 AATGTGCCGGGGGTCCTAAGACCCATAACCCTAGTGGCGTACGAGAAGATGACCCCCCAG 1083

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140

Db       1084 TCAATCCTGACCGTGGCTGGCGTATCCAACTATGAGCTGATCCCAAACCCAGACCTACTG 1143

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200

Db       1144 AAGAACATGGTCACCAAGTATGGAAAGTATGACCCTGAGGGCCTCAACTATGCCAAGATG 1203

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260

Db       1204 ATCCTGTCCCACAGAGAGGAGCTGGACATTAGAACCGTCTGGAGGACTGAGGAATACAAA 1263

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320

Db       1264 GAAAGGACAAGAGCATTCAAAGAGATCACTGACTTCACAAGTGACCTACCAACCTCAAAG 1323

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAA 1359

Db       1324 GCATGGGGATGGAGGGACCTGGTCAGAGGCATCAGAAAA 1362
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RESULT 9
AAZ50081
ID   AAZ50081 standard; DNA; 780 BP.
XX
AC   AAZ50081;
XX
DT   04-MAY-2000  (first entry)
XX
DE   Infectious pancreatic necrosis virus surface glycoprotein DNA.
XX
KW   Surface layer protein; S-layer secretion signal; antibiotic; vaccine;
KW   recombinant fusion protein cleavage; enzyme; protein polymer; foodstuff;
KW   antibacterial enzyme; surface glycoprotein; salmonid virus; IPNV; ds.
XX
OS   Infectious pancreatic necrosis virus.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     1. .780
FT                   /*tag= a
FT                   /product= "Surface glycoprotein"
XX
PN   WO200004170-A1.
XX
PD   27-JAN-2000.
XX
PF   14-JUL-1999;   99WO-CA000637.
XX
PR   14-JUL-1998;   98CA-02237704.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Smit J;
XX
DR   WPI; 2000-182434/16.
DR   P-PSDB; AAY44759.
XX
PT   Cleavage of Caulobacter produced recombinant fusion proteins useful for
PT   producing vaccine peptides.
XX
PS   Example 2; Page 25; 33pp; English.
XX
CC   The patent discloses a method for cleaving a recombinant fusion protein
CC   which is produced by Caulobacter and consists of Caulobacter surface
CC   layer (S-layer) protein (containing the C-terminal secretion signal) and
CC   a target protein heterologous to Caulobacter. The cleavage of target
CC   protein from the S-layer protein is carried out under mild acid
CC   conditions so that cleavage occurs at aspartate-proline dipeptide site
CC   without solubilising the protein. The cleavage is accomplished while the
CC   fusion protein is in an insoluble aggregate form which facilitates
CC   purification of the protein. The method is useful for producing pure
CC   proteins including recombinant human and animal therapeutic antibiotic
CC   and vaccine peptides, enzymes, protein polymers, and antibacterial
CC   enzymes for foodstuffs. The present sequence is a DNA encoding surface
CC   glycoprotein, a vaccine candidate, from Infectious pancreatic necrosis
CC   virus (IPNV). DNA encoding a fragment of the glycoprotein from amino
CC   acids 145-257 was fused to DNA sequence specifying two putative T-cell
CC   activating epitopes, MVF and P2. This chimeric protein was in turn fused
CC   to DNA encoding C. crescentus S- layer secretion signal (corresponds to
CC   the C-terminal portion of S-layer protein from amino acid 690 onwards)
CC   for construction of a recombinant fusion construct which is expressed in
CC   Caulobacter and then cleaved to recover the vaccine candidate protein
XX
SQ   Sequence 780 BP; 224 A; 234 C; 191 G; 131 T; 0 U; 0 Other;
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  Query Match             53.3%;  Score 753;  DB 3;  Length 780;
  Best Local Similarity   98.1%;  Pred. No. 3.6e-201;
  Matches  762;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60

Db          4 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 63

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120

Db         64 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACAAGAGACCTCGTCATAC 123

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180

Db        124 AACTTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 183

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240

Db        184 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 243

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300

Db        244 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 303

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360

Db        304 AAATACGACATTCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 363

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420

Db        364 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAATAGCCTG 423

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480

Db        424 ATGTCCCTAACTACGAACCCCCAGGACAAAGCCAACAACCAGCTGGTGACCAAAGGAGTC 483

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
```

```
Db        484 ACCGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 543

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        544 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAGGATGAGGTGCACAGCTGCAATTGCACCA 603

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        604 CGGAGGTACGAGATCGACCTCCCATCCCAAAGCCTACCCCCCGTTCCTGCGACAGGAACC 663

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        664 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAGCTCCACAACAGTGACGGGAGAC 723

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTG 777
              ||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db        724 ATAAACTTCAGTCTGGCAGAACGACCCGCAAACGAGACCAGGTTCGACTTCCAGCTG 780


RESULT 10
AAV26606
ID   AAV26606 standard; cDNA; 3264 BP.
XX
AC   AAV26606;
XX
DT   17-OCT-2003  (revised)
DT   28-AUG-1998  (first entry)
XX
DE   Plasmid pUC18FLA23 containing IBDV segment A cDNA.
XX
KW   Plasmid pUC18FLA23; IBDV; Gumboro disease; vaccine;
KW   synthetic RNA transcript; reverse genetics; VP2; VP3; VP4; VP5; ss;
KW   cyclic; circular.
XX
OS   Infectious bursal disease virus; strain 23/82.
XX
FH   Key             Location/Qualifiers
FT   CDS             97. .534
FT                   /*tag=  a
FT                   /product= "VP5"
FT   CDS             131. .3172
FT                   /*tag=  b
FT                   /product= "VP2-VP4-VP3"
XX
PN   WO9809646-A1.
XX
PD   12-MAR-1998.
XX
PF   31-JUL-1997;   97WO-US012955.
XX
PR   05-SEP-1996;   96US-00708541.
XX
PA   (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI   Vakharia VN,  Mundt E;
XX
DR   WPI; 1998-193322/17.
DR   P-PSDB; AAW54376, AAW54377.
XX
PT   Generation of live birna:virus from synthetic RNA transcripts - useful
PT   for vaccines against infectious bursal disease.
XX
PS   Example 1; Fig 6A-B; 84pp; English.
XX
CC   Plasmid pUC18FLA23 contains infectious bursal disease virus (IBDV) strain
CC   23/82 segment A cDNA that encodes polyprotein VP2-VP4-VP3 (see AAW54377)
CC   and the newly identified non-structural protein VP5 (see AAW54376). It
CC   was obtained by RT-PCR amplification (see AAV26596-99) of strain 23/82
CC   RNA and cloning into vector pUC18. In a new reverse genetics system for
CC   IBDV, 3 independent full-length cDNA clones (see also AAV26604 and
CC   AAV26605) were constructed which contain segment A of serotype I strain
CC   D78 or serotype II strain 23/82 and segment B of the serotype I strain
CC   P2. Synthetic RNAs of segments A and B were produced by in vitro
CC   transcription of linearised plasmids with T7 RNA polymerase. Transfection
CC   of Vero cells with combined plus strand transcripts of both segments
CC   generated infectious virus. The development of a reverse genetics system
CC   for double-stranded RNA viruses will facilitate studies of the regulation
CC   of viral gene expression pathogenesis, and design of a new generation of
CC   live and inactivated vaccines. (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 3264 BP; 834 A; 942 C; 853 G; 635 T; 0 U; 0 Other;

  Query Match           18.6%;  Score 262.6;  DB 2;  Length 3264;
  Best Local Similarity  52.6%;  Pred. No. 6.9e-63;
  Matches  724;  Conservative    0;  Mismatches  629;  Indels   24;  Gaps    6;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
              | |  || | |||  ||| ||||| ||  ||| ||||||||||     |||||  ||||
Db        181 CCTTCTGATGCCAACGACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 240

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
               || |     || |||||| | |||||| |     ||    ||  ||||    ||  |  |
Db        241 ACTCAGGTCCGAAACCTCGACTTACAACTTGACTGTAGGGGATACAGGGTCAGGACTAAT 300

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
              ||| | |||||||||     || || |||     | ||||| ||||||| |  | |   ||
Db        301 TGTCTTTTTCCCTGGATTCCCTGGTTCAGTTGTAGGTGCTCACTACACACTGCA---GAG 357

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
              |      |        | |||||||||  |||   |||  ||||| |||||         ||
Db        358 CAGTGGGAACTACCAATTCGACCAGATGCTCCTGACAGCGCAGAACCTGCCTGCCAGCTA 417

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
              ||||||| | |||||  |    ||||        | | |       ||||||  || |  ||
Db        418 CAACTACTGCAGGCTAGTGAGCAGGAGTCTAACCGTACGGTCAAGCACACTCCCTGGTGG 477

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
              | ||||| || ||||| ||  | |||||  |  |||||| | || || |||  |||| |
Db        478 CGTTTATGCACTAAACGGAACCATAAACGCAGTGACCTTCCACGGAAGCCTGAGTGAGTT 537

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
              |      |  | |||||||  | ||||||||    ||  |||||  | | |||||  ||
Db        538 GACTGACTACAGCTACAACGGGCTGATGTCAGCCACTGCGAACATCAACGACAAGATCGG 597

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
              |||   || ||      |||| || || || || | |||||| ||     |  |||
Db        598 GAACGTTCTAGTTGGAGAAGGGGTGACTGTTCTCAGTCTACCGACTTCATATGACCTTAG 657

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
              || ||  | || |  |||   | |||      || ||| |  | | |      |||||
Db        658 TTATGTGAGACTCGGTGACCCCATCCCCGCAGCAGGACTCGACCCGAAGTTGATGGCCAC 717

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
              |      | |  |      |      |                |      || ||||
Db        718 GTGCGACAGTAGTGACAGACCCAGAGTCTACACCATAACAGCTGCAGATGAATACCAATT 777

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              |    | |  |     |||  ||        ||||| || | |   |  |||  |||
Db        778 CTCGTCACAACTCATCCCGAGTGGCGTGAAGACCACACTGTTCTCCGCCAACATCGATGC 837

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
              |||  |  |  |  ||    || ||  |  |||||| |      ||  | |     |
Db        838 TCTCACCAGCTTCAGCGTTGGTGGTGAGCTTGTCTTCAGCC------AAGTAACGATCCA 891

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGAC---AACGACGTCCCAGT 809
                |  | ||| ||      | |||||| ||  |||||   | |||||  ||||
Db        892 AAGCATTGAAGTGGACGTCACCATTCACTTCATTGGGTTTGACGGGACAGACGTAGCAGT 951

Qy        810 TGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAA 869
              ||||  |  |  |  |  |  |||| ||  |  |||     ||  ||  |||
Db        952 CAAGGCAGTTGCAACAGACTTTGGGCTGACAACTGGGACAAACAACCTTGTGCCATTCAA 1011

Qy        870 GATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTC 929
                 || |   |||| ||  |  | |||||  |||| |||||     | || ||
Db       1012 ------CCTGGTGGTCCCAACAAATGAGATCACCCAGCCCATCACTTCCATGAAACTAGA 1065
```

```
Qy        930 ATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCC 989
Db       1066 GGTTGTGACCTACAAGATTGGCGGCACCGCTGGTGACCCAATATCATGGACAGTGAGTGG 1125

Qy        990 AGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCAC 1049
Db       1126 TACAC---TAGCTGTGACGGTGCACGGAGGCAACTACCCTGGGGCTCTCCGTCCTGTCAC 1182

Qy       1050 ACTGGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAA 1109
Db       1183 CCTGGTGGCCTATGAACGAGTGGCTGCAGGATCTGTTGTCACAGTTGCAGGGGTGAGCAA 1242

Qy       1110 CTACGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTA 1169
Db       1243 CTTCGAGCTAATCCCCAACCCTGAGCTTGCAAAGAACCTAGTTACAGAGTATGGCCGCTT 1302

Qy       1170 CGACCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACAT 1229
Db       1303 TGACCCCGGAGCAATGAACTACACCAAACTAATACTGAGTGAGAGAGATCGTCTAGGCAT 1362

Qy       1230 CAGGACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCAC 1289
Db       1363 CAAGACAGTCTGGCCCACCAGGGAGTACACCGATTTCAGGGAGTACTTCATGGAGGTTGC 1422

Qy       1290 GGACTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGG 1349
Db       1423 AGATCTCAACTCACCCCTAAAGATTGCAGGAGCATTTGGCTTTAAGGACATAATCCGAGC 1482

Qy       1350 AATTCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
Db       1483 CATTCGGAAGATTGCGGTGCCAGTGGTATCCACACTCTTCCCTCCAGCTGCACCCCT 1539
```

RESULT 11
AAF25059
ID AAF25059 standard; cDNA; 3260 BP.
XX
AC AAF25059;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of the A-segment of an IBDV isolate.
XX
KW IBDV; vaccine; infectious bursal disease; IBD; poultry; chicken; duck;
KW rooster; hen; broiler; roaster; breeder; layer; turkey; ss.
XX
OS Infectious bursal disease virus.
XX
PN EP1069187-A1.
XX
PD 17-JAN-2001.
XX
PF 14-JUL-1999; 99EP-00202316.
XX
PR 14-JUL-1999; 99EP-00202316.
XX
PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX
DR WPI; 2001-184296/19.
XX
PT New infectious recombinant Infectious Bursal Disease Virus, useful as a
PT vaccine for preventing subclinical and clinical infectious bursal disease
PT in poultry, e.g. chickens, broilers, roasters, breeders, layers, turkeys
PT or ducks.
XX
PS Disclosure; Page 38-39; 90pp; English.
XX
CC The specification describes an infectious recombinant Infectious Bursal
CC Disease Virus (IBDV). This recombinant virus is incapable of growing in a
CC non-bursa-cell or in a cell derived from it. The recombinant IBDV is
CC useful as a vaccine for preventing subclinical and clinical infectious
CC bursal disease (IBD). It is particularly useful for preventing IBD in
CC poultry anytime before or after hatching. Poultry includes chickens,
CC roosters, hens, broilers, roasters, breeders, layers, turkeys or ducks.
CC The present sequence represents the cDNA sequence of the A-segment of an
CC IBDV isolate
XX
SQ Sequence 3260 BP; 798 A; 839 C; 813 G; 571 T; 0 U; 239 Other;

Query Match 17.4%; Score 246; DB 4; Length 3260;
Best Local Similarity 49.5%; Pred. No. 3.2e-58;
Matches 680; Conservative 34; Mismatches 639; Indels 21; Gaps 5;

```
Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
Db        181 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTRGAGAAGCACAC 240

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
Db        241 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 300

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
Db        301 TGTCTTTTTCCCTGGWTTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 357

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
Db        358 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGYTA 417

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
Db        418 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTGAGGTCAAGCACACTYCCTGGTGG 477

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
Db        478 CGTTTATGCACTAAAYGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 537

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
Db        538 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATYGG 597

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
Db        598 GAACGTCCTAGTAGGGGAAGGGGTMACCGTCCTCAGCTTACCCACATCATATGATCTTGG 657

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
Db        658 GTATGTGAGRCTYGGTGACCCCATTCCCGCWATAGGGCTYGACCCAAAAATGGTAGCMAC 717

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
Db        718 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATGATTACCAATT 777

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
Db        778 CTCATCACAGTACCAASCAGGTGGGGTAACAATCACACTGTTCTCAGCYAAYATYGATGC 837

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
Db        838 CATCACAAGCCTCAGCRTYGGGGGAGARCTCGTGTTTCAAACAAGCGTCCAMGGCCTTRT 897

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
Db        898 ACTGGGYGCYACCATCTACCTYATAGGCTTTGATGGGACWGCGGTAATCACCAGRGCTGT 957

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
Db        958 GGCCGCARACAATGGGCTRACGRCCGGCACYGACAACCTTWTGCCATTCAATMTTGTGAT 1017

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
Db       1018 TCCAACMARCGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTC 1074

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
```

```
Db       1075 CAA----AAGTGGTGGTCAGGCRGGGGATCAGATGTCRTGGTCRGCAAGWGGGAGCC--- 1127

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052

Db       1128 -----TAGCAGTGACGATCCAYGGTGGCAACTATCCAGGGGCCCTCCGTCCCGTCACRCT 1182

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112

Db       1183 AGTRGCCTACGAAAGAGTGGCAACAGGATCYGTCGTTACGGTCGCYGGGGTGAGCAACTT 1242

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172

Db       1243 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTYACAGAATACGGCCGATTTGA 1302

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232

Db       1303 CCCAGGAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGTCTTGGCATCAA 1362

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292

Db       1363 GACCGTMTGGCCAACAAGGGAGTACACTGACTTTCGYGARTACTTCATGGAGGTGGCCGA 1422

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352

Db       1423 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTYGGCTTCAAAGACATAATCCGGGCCMT 1482

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406

Db       1483 AAGGAGGATAGCTGTGCCGGTGGTCTCYACAYTGTTCCCACCYGCCGCTCCCCT 1536
```

RESULT 12
AAT63072
ID AAT63072 standard; DNA; 1471 BP.
XX
AC AAT63072;
XX
DT 25-MAR-2003 (revised)
DT 12-MAY-1997 (first entry)
XX
DE DNA sequence encompassing clone E/DEL-2.
XX
KW Infectious bursal disease virus; IBDV; large segment; GLS 5 strain;
KW structural protein; VP2; VP3; VP4; immunogen; vaccine; Gumboro disease;
KW ss.
XX
OS Infectious bursal disease virus.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .18
FT		/*tag= a
FT	CDS	19. .1470
FT		/*tag= b

XX
PN US5595912-A.
XX
PD 21-JAN-1997.
XX
PF 23-MAR-1994; 94US-00216276.
XX
PR 04-MAY-1990; 90US-00519202.
PR 28-JUN-1993; 93US-00083784.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Snyder D, Vakharia V;
XX
DR WPI; 1997-107584/10.
DR P-PSDB; AAW14744, AAW14745.
XX
PT Infectious bursal disease virus nucleic acids - for prodn. of vaccines
PT for poultry for protection against Gumboro disease.
XX
PS Example 12; Col 17-20; 41pp; English.
XX
CC This sequence represents a fragment of the infectious bursal disease
CC virus (IBDV) large segment from the E/DEL strain. This sequence contains
CC a coding sequence derived from the structural protein genes VP2, VP3 and
CC VP4. The proteins encoded by this sequence, esp. VP2 which is the major
CC host protective immunogen of IBDV, may be used to prepare vaccines
CC against IBDV infection/Gumboro disease. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 1471 BP; 403 A; 385 C; 368 G; 315 T; 0 U; 0 Other;

Query Match 17.0%; Score 240.6; DB 2; Length 1471;
Best Local Similarity 51.1%; Pred. No. 7.6e-57;
Matches 701; Conservative 0; Mismatches 649; Indels 21; Gaps 5;

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Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95

Db        102 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 161

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155

Db        162 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 221

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215

Db        222 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 278

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275

Db        279 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 338

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335

Db        339 CAACTACTGGAGGCTAGTGAGTTGGAGTCTCACAGTAAGGTCAAGCACAGTCCCTGGTGG 398

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395

Db        399 CCTTTATGCACTAAACGGCACCATAAACGCGGTGACCTTCCAAGGAAGCCTGAGTGAACT 458

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455

Db        459 GACAGATGTTAGCTACAACGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 518

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515

Db        519 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATGTTGG 578

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572

Db        579 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 638

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632

Db        639 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATAATTACCAATT 698

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692

Db        699 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 758

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752

Db        759 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAACAAGCGTCCAAAGCCTTGT 818

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812

Db        819 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 878

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872

Db        879 GGCCGCAAACAATGGGCTGACGGCCGGCATCGACAATCTTATGCCATTCAATCTTGTGAT 938

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
```

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Db        939 TCCAACCAATGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTC 995

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992

Db        996 CAAAAGTGATGGTCAGGCAGG----GGAACAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1051

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052

Db       1052 CAGTGACGATCCATGGT--------GGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1103

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112

Db       1104 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1163

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172

Db       1164 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATATGGCCGATTTGA 1223

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232

Db       1224 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCGCCTTGGCATCAA 1283

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292

Db       1284 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1343

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352

Db       1344 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1403

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACC 1403

Db       1404 AAGGAGGATAGCTGTACCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCC 1454


RESULT 13
AAQ45441
ID   AAQ45441 standard; DNA; 3180 BP.
XX
AC   AAQ45441;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   07-OCT-1994  (first entry)
XX
DE   Sequence of wild type Delaware infectious bursal disease virus (IBDV).
XX
KW   Infectious bursal disease virus; IBDV; vaccine;
KW   monoclonal antibody Mab 67; assay; ss.
XX
OS   Infectious bursal disease virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             64. .3102
FT                   /*tag= a
XX
PN   WO9406475-A1.
XX
PD   31-MAR-1994.
XX
PF   01-SEP-1993;   93WO-US008033.
XX
PR   15-SEP-1992;   92US-00944525.
XX
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI   Snyder DB,  Vakharia V,  Luetticken HD;
XX
DR   WPI; 1994-118171/14.
DR   P-PSDB; AAR51171.
XX
PT   Attenuated live vaccine for Delaware strain infectious bursal disease
PT   virus - is produced by screening with a monoclonal antibody and used for
PT   immunising poultry against IBDV.
XX
PS   Claim 9; Fig 1A-1K; 24pp; English.
XX
CC   The applicants have developed a Mab, designated Mab 67, which neutralises
CC   wild-type Delaware strain IBDV. It was developed according to the method
CC   set forth in US Patent 4,956,452. The hybridoma cell line expressing Mab
CC   67 has been deposited under ATCC- HB111222. Bps 1-1404 of AAQ45441 is the
CC   nucleotide sequence of the gene responsible for the expression of
CC   Delaware IBDV structural protein(s) recognised by Mab 67. Mab 67 can be
CC   used in an assay to determine the presence of Delaware type IBDV and can
CC   be employed to prepare a vaccine conferring challenge protection against
CC   Delaware- type IBDV. (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 3180 BP; 864 A; 880 C; 822 G; 614 T; 0 U; 0 Other;

  Query Match            16.9%;  Score 238.8;  DB 2;  Length 3180;
  Best Local Similarity   51.0%;  Pred. No. 3.4e-56;
  Matches  701;  Conservative    0;  Mismatches  652;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95

Db        114 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 173

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155

Db        174 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 233

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215

Db        234 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 290

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275

Db        291 CAGTGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 350

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335

Db        351 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 410

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395

Db        411 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 470

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455

Db        471 GACAGATGTTAGCTACAACGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 530

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515

Db        531 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATCTTGG 590

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572

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Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632

Db        651 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAAGTGCAGCCGATAATTACCAATT 710

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692

Db        711 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 770

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752

Db        771 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAAGAAGCGTCCAAAGCCTTGT 830

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812

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Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
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Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
Db        951 TCCAACCAATGAGATAACCCAGCCAATCACA---TCCATCATACTGGAGATAGTGACCTC 1007

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
Db       1008 CAAAAGTGATGGTCAGGCAGG----GGAACAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1063

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
Db       1064 CAGTGACGATCCATGGT--------GGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1115

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
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Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
Db       1236 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCACCTTGGCATCAA 1295

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
Db       1296 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1355

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
Db       1356 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1415

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
Db       1416 AAGGAGGATAGCTGTACCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCCTCT 1469


RESULT 14
AAT05623
ID   AAT05623 standard; cDNA; 3230 BP.
XX
AC   AAT05623;
XX
DT   16-OCT-2003  (revised)
DT   15-FEB-1996  (first entry)
XX
DE   IBDV GLS structural protein fragment cDNA.
XX
KW   IBDV; immunogen; vaccine; poultry; ss.
XX
OS   Infectious bursal disease virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             114. .3152
FT                   /*tag=  a
FT                   /product= "VP2/VP4/VP3 structural protein fragment"
XX
PN   WO9526196-A1.
XX
PD   05-OCT-1995.
XX
PF   29-MAR-1995;   95WO-US003772.
XX
PR   29-MAR-1994;   94US-00219262.
XX
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI   Vakharia V,  Snyder DB,  Mengel-Whersat SA;
XX
DR   WPI; 1995-351197/45.
DR   P-PSDB; AAR85439.
XX
PT   Chimeric infectious bursal disease virus polypeptide immunogens -
PT   comprising VP2 with modified epitopic amino acid sequence for preparation
PT   of vaccines for immunisation of poultry.
XX
PS   Disclosure; Fig 5A-K; 77pp; English.
XX
CC   A cDNA clone contg. the entire coding region of the large RNA segment of
CC   infectious bursal disease virus serotype I strain GLS has the sequence
CC   given in AAT05623, and encodes the structural proteins VP2/4/3 (in that
CC   order). Chimeric immunogens in which an epitopic determinant of a lethal
CC   IBDV strain is inserted into GLS VP2 can be expressed in recombinant
CC   mammalian and poultry host cells. (Updated on 16-OCT-2003 to standardise
CC   OS field)
XX
SQ   Sequence 3230 BP; 865 A; 908 C; 838 G; 619 T; 0 U; 0 Other;

  Query Match            16.9%;  Score 238.8;  DB 2;  Length 3230;
  Best Local Similarity  51.0%;  Pred. No. 3.4e-56;
  Matches  701;  Conservative    0;  Mismatches  652;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
Db        164 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 223

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
Db        224 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 283

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
Db        284 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 340

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
Db        341 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 400

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
Db        401 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 460

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
Db        461 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 520

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
Db        521 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 580

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
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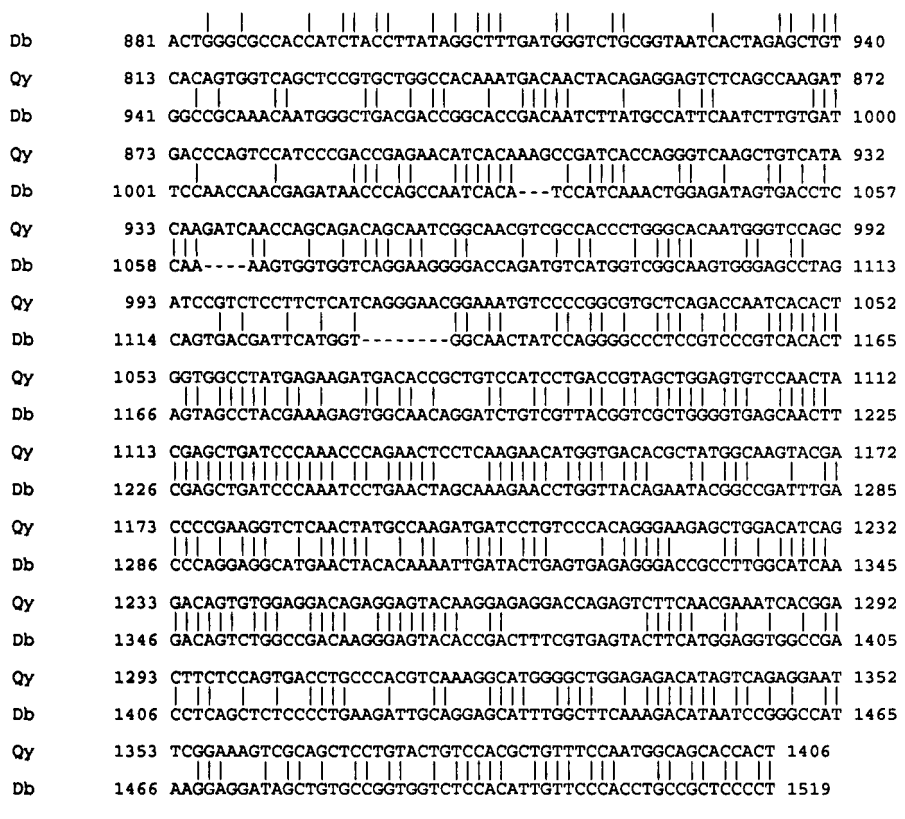
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Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
Db        701 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCTGATGATTACCAATT 760

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
Db        761 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACCCTGTTCTCAGCCAACATTGATGC 820

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
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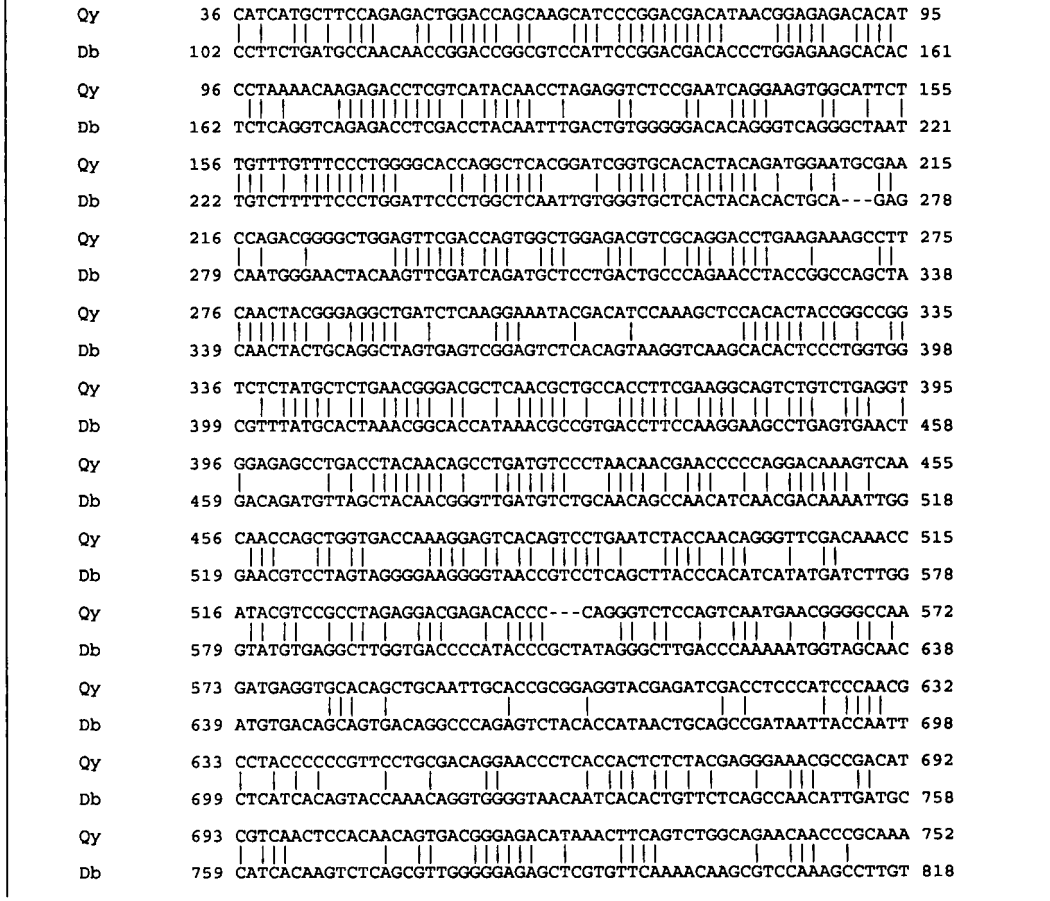
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RESULT 15
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ID AAQ14896 standard; DNA; 1471 BP.
XX
AC AAQ14896;
XX
DT 27-AUG-2003 (revised)
DT 24-FEB-1992 (first entry)
XX
DE E/DEL-2 clone.
XX
KW Infectious bursal disease virus; IBDV; vaccine; poultry; ss.
XX
OS Infectious bursal disease virus.
XX
FH Key Location/Qualifiers
FT CDS 19. .1470
FT /*tag= a
FT /note= "polypeptide encoded by E/DEL-2 clone"
XX
PN WO9116925-A.
XX
PD 14-NOV-1991.
XX
PF 04-MAY-1990; 90US-00519202.
XX
PR 04-MAY-1990; 90US-00519202.
XX
PA (UYMA-) UNIV MARYLAND COL.

XX
PI Vakharia V;
XX
DR WPI; 1991-353531/48.
DR P-PSDB; AAR15053.
XX
PT Infectious bursal disease virus nucleic acids - useful as vaccines
PT against IBDV in poultry.
XX
PS Example; Page 28; 45pp; English.
XX
CC The sequence is that of a clone of variant Delaware type E of infectious
CC bursal disease virus (IBDV). It can be used in broad spectrum IBDV
CC poultry vaccines, administration is ophthalmically, by injection, nasally
CC or orally, at any time after hatching and as a booster at other times.
CC Poultry treated include chickens, roosters, broilers, roasters, breeders,
CC layers, turkeys and ducks. See also AAQ14897. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 1471 BP; 403 A; 389 C; 366 G; 313 T; 0 U; 0 Other;

Query Match 16.8%; Score 237.4; DB 2; Length 1471;
Best Local Similarity 51.0%; Pred. No. 6e-56;
Matches 699; Conservative 0; Mismatches 651; Indels 21; Gaps 5;



```
Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
Db        819 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 878

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
Db        879 GGCCGCAAACAATGGGCTGACGGCCGGCATCGACAATCTTATGCCATTCAATCTTGTGAT 938

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
Db        939 TCCAACCAATGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTC 995

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
Db        996 CAAAAGTGATGGTCAGGCAGG----GGAACAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1051

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
Db       1052 CAGTGACGATCCATGGT--------GGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1103

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
Db       1104 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1163

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
Db       1164 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATATGGCCGATTTGA 1223

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
Db       1224 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCGCGTTGGCATCAA 1283

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
Db       1284 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1343

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
Db       1344 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1403

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACC 1403
Db       1404 AAGGAGGATAGCTGTACCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCC 1454
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1413	100.0	1485	7	US-10-733-031-6	Sequence 6, Appli
3	1403.4	99.3	1527	10	US-11-083-175-5	Sequence 5, Appli
4	1403.4	99.3	3069	10	US-11-083-175-13	Sequence 13, Appl
5	1390.6	98.4	3097	5	US-10-216-981A-2	Sequence 2, Appli
6	246	17.4	3260	6	US-10-046-671B-70	Sequence 70, Appl
7	233.8	16.5	3004	6	US-10-377-718-2	Sequence 2, Appli
8	233.8	16.5	3004	6	US-10-429-735-2	Sequence 2, Appli
9	232.4	16.4	3260	6	US-10-046-671B-71	Sequence 71, Appl
10	232	16.4	3260	6	US-10-046-671B-72	Sequence 72, Appl
11	223.4	15.8	1374	3	US-09-964-895-1	Sequence 1, Appli
12	223.4	15.8	1374	8	US-10-832-353-1	Sequence 1, Appli
13	216.4	15.3	3054	3	US-09-477-574A-1	Sequence 1, Appli
14	214.2	15.2	1362	3	US-09-784-990-13	Sequence 13, Appl
15	214.2	15.2	1362	6	US-10-229-412-13	Sequence 13, Appl
16	214.2	15.2	1374	3	US-09-964-895-16	Sequence 16, Appl
17	214.2	15.2	1374	8	US-10-832-353-16	Sequence 16, Appl
18	207.6	14.7	1425	8	US-10-839-509-11	Sequence 11, Appl
19	206	14.6	1368	8	US-10-839-509-10	Sequence 10, Appl
20	112.2	7.9	1078	3	US-09-888-876-1	Sequence 1, Appli
c 21	45.4	3.2	154817	6	US-10-085-117-334	Sequence 334, App
22	45	3.2	1965	6	US-10-369-493-28400	Sequence 28400, A
23	45	3.2	1965	6	US-10-369-493-31160	Sequence 31160, A
24	44.8	3.2	4565	7	US-10-476-397-18	Sequence 18, Appl
25	43.8	3.1	506	6	US-10-029-386-20619	Sequence 20619, A
c 26	43.8	3.1	1168	6	US-10-017-161-2179	Sequence 2179, Ap
27	43.8	3.1	1776	6	US-10-369-493-37683	Sequence 37683, A
28	43.4	3.1	1493	6	US-10-029-386-25133	Sequence 25133, A
29	42.4	3.0	1078	7	US-10-437-963-46906	Sequence 46906, A
c 30	42.2	3.0	1168	6	US-10-292-798-1825	Sequence 1825, Ap
31	41.6	2.9	793	8	US-10-425-115-46860	Sequence 46860, A
32	41	2.9	488	3	US-09-918-995-626	Sequence 626, App
33	41	2.9	1622	7	US-10-437-963-57176	Sequence 57176, A
c 34	40.2	2.8	3145	10	US-11-097-143-33601	Sequence 33601, A
c 35	39.2	2.8	581	6	US-10-029-386-12634	Sequence 12634, A
36	39.2	2.8	983	3	US-09-864-761-21172	Sequence 21172, A
37	39.2	2.8	1128	5	US-10-225-567A-202	Sequence 202, App
38	39.2	2.8	1128	7	US-10-181-906-11	Sequence 11, Appl
39	39.2	2.8	1180	6	US-10-305-720-1061	Sequence 1061, Ap
40	39.2	2.8	1407	8	US-10-411-910A-215	Sequence 215, App
41	39.2	2.8	1673	9	US-10-512-455-1	Sequence 1, Appli
42	39.2	2.8	1959	3	US-09-864-761-4424	Sequence 4424, Ap
43	39.2	2.8	1972	6	US-10-017-161-1981	Sequence 1981, Ap
44	39.2	2.8	1972	6	US-10-292-798-1629	Sequence 1629, Ap
45	39	2.8	2265	6	US-10-156-761-4285	Sequence 4285, Ap

ALIGNMENTS

RESULT 1
US-10-733-031-5
; Sequence 5, Application US/10733031
; Publication No. US20040175441A1
; GENERAL INFORMATION:
; APPLICANT: BOOTLAND, LINDA M.
; APPLICANT: BEIFUSS, KATHERINE
; APPLICANT: JILKA, JOSEPH
; APPLICANT: LIZAMA, MALCOLM L.
; APPLICANT: LAMPHEAR, BARRY
; APPLICANT: STREATFIELD, STEPHEN
; TITLE OF INVENTION: IMMUNIZATION OF FISH WITH PLANT-EXPRESSED RECOMBINANT
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 10044
; CURRENT APPLICATION NUMBER: US/10/733,031
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 60/433,381
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Infectious pancreatic necrosis virus
US-10-733-031-5

Query Match 100.0%; Score 1413; DB 7; Length 1413;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
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Db          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Qy       241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
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Db       241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300

Qy       301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360

Qy       361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420

Qy       421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
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Db       421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480

Qy       481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540

Qy       541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600

Qy       601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660

Qy       661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720

Qy       721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780

Qy       781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840

Qy       841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900

Qy       901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960

Qy       961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
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Db       961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020

Qy      1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080

Qy      1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
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Db      1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140

Qy      1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200

Qy      1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
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Db      1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260

Qy      1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320

Qy      1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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Db      1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380

Qy      1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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Db      1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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RESULT 2
US-10-733-031-6
; Sequence 6, Application US/10733031
; Publication No. US20040175441A1
; GENERAL INFORMATION:
; APPLICANT: BOOTLAND, LINDA M.
; APPLICANT: BEIFUSS, KATHERINE
; APPLICANT: JILKA, JOSEPH
; APPLICANT: LIZAMA, MALCOLM L.
; APPLICANT: LAMPHEAR, BARRY
; APPLICANT: STREATFIELD, STEPHEN
; TITLE OF INVENTION: IMMUNIZATION OF FISH WITH PLANT-EXPRESSED RECOMBINANT
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 10044
; CURRENT APPLICATION NUMBER: US/10/733,031
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 60/433,381
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-733-031-6

Query Match 100.0%; Score 1413; DB 7; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
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Db        73 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 132

Qy        61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       133 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 192

Qy       121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       193 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 252

Qy       181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       253 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 312

Qy       241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       313 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 372

Qy       301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       373 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 432

Qy       361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       433 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 492

Qy       421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       493 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 552

Qy       481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
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Db       553 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 612
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Qy       541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Db       613 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 672

Qy       601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
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Db       673 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 732

Qy       661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       733 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 792

Qy       721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       793 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 852

Qy       781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
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Db       853 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 912

Qy       841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       913 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 972

Qy       901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       973 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1032

Qy       961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1033 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1092

Qy      1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1093 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1152

Qy      1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
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Db      1153 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1212

Qy      1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1213 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1272

Qy      1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1273 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1332

Qy      1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
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Db      1333 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1392

Qy      1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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Db      1393 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1452

Qy      1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
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Db      1453 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1485
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RESULT 3
US-11-083-175-5
; Sequence 5, Application US/11083175
; Publication No. US20050163795A1
; GENERAL INFORMATION:
; APPLICANT: Simard, Nathalie C.
; APPLICANT: Bootland, Linda M.
; TITLE OF INVENTION: IHNV G Protein For Immune Stimulation
; FILE REFERENCE: H-32647
; CURRENT APPLICATION NUMBER: US/11/083,175
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/EP03/010305
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: GB0221552.3
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: GB0221553.1
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: IPNV
US-11-083-175-5

Query Match 99.3%; Score 1403.4; DB 10; Length 1527;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy         1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
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Db         4 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 63

Qy        61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
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Db        64 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 123

Qy       121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
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Db       124 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 183

Qy       181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Db       184 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 243

Qy       241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
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Db       244 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 303

Qy       301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       304 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 363

Qy       361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       364 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 423

Qy       421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       424 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 483

Qy       481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       484 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 543

Qy       541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       544 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAACTGCACCG 603

Qy       601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       604 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 663

Qy       661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
             ||||| |||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db       664 CTCACTACTCTCTACGCGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 723

Qy       721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       724 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 783

Qy       781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       784 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 843
```

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Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 903

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 963

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1023

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1083

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1143

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1203

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1204 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1263

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1264 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1323

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1383

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
              |||||||||||||||||||||||||||||| |||
Db       1384 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1416
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RESULT 4
US-11-083-175-13
; Sequence 13, Application US/11083175
; Publication No. US20050163795A1
; GENERAL INFORMATION:
; APPLICANT: Simard, Nathalie C.
; APPLICANT: Bootland, Linda M.
; TITLE OF INVENTION: IHNV G Protein For Immune Stimulation
; FILE REFERENCE: H-32647
; CURRENT APPLICATION NUMBER: US/11/083,175
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/EP03/010305
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: GB0221552.3
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: GB0221553.1
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3069
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding IHNV G protein IPNV VP2 fusion
; OTHER INFORMATION: protein with linker
US-11-083-175-13

Query Match 99.3%; Score 1403.4; DB 10; Length 3069;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1546 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 1605

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1606 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 1665

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1666 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 1725

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 1785

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1786 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 1845

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 1905

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1906 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 1965

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1966 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 2025

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2026 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 2085

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       2086 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAACTGCACCG 2145

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2146 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 2205

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 CTCACTACTCTCTACGCGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 2265

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 2325

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 2385

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 2445

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 2505

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 2565

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 2625
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Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 2685

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 2745

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2746 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 2805

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2806 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 2865

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2866 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 2925

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
             |||||||||||||||||||||||||||| |||
Db       2926 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 2958


RESULT 5
US-10-216-981A-2
; Sequence 2, Application US/10216981A
; Publication No. US20030072772A1
; GENERAL INFORMATION:
;  APPLICANT: VIKHARIA, VIKRAM N
;  TITLE OF INVENTION: SUB-UNIT VACCINE FOR INFECTIOUS PANCREATIC NECROSIS VIRUS
;  FILE REFERENCE: 4115-154
;  CURRENT APPLICATION NUMBER: US/10/216,981A
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: 60/311,488
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 3097
;   TYPE: DNA
;   ORGANISM: Infectious pancreatic necrosis virus
US-10-216-981A-2

  Query Match             98.4%;  Score 1390.6;  DB 5;  Length 3097;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1399;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||| |||||||||||||||||||| |||||||||| ||||||||||||||||||||||
Db        122 AACACAAACAAGGCAACCGCAACTTACCTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        182 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACAAGAGACCTCGTCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AACTTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 301

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AAATATGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAACTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTACTGCGACAGGAACC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        782 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACGACAGTGACGGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||
Db        842 ATAAACTTCAGTCTGACAGAACAACCCGCAGTCGAGACCAAGTTCGACTTCCAGCTGGAC 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTA 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1441

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
              |||||||||||||||||||||||||||| |||
Db       1502 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1534
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RESULT 6
US-10-046-671B-70
; Sequence 70, Application US/10046671B
; Publication No. US20030152592A1
; GENERAL INFORMATION:
;  APPLICANT: Boot, Hendrik J.
;  APPLICANT:  Huurne ter, Anna A.H.M
;  APPLICANT:  Peeters, Bernardus P.H.
;  TITLE OF INVENTION: Mosaic Infectious Bursal Disease Virus Vaccines
;  FILE REFERENCE: 2183-5238US
;  CURRENT APPLICATION NUMBER: US/10/046,671B
;  CURRENT FILING DATE:  2002-01-14
;  PRIOR APPLICATION NUMBER: PCT/NL00/00493
;  PRIOR FILING DATE: 2000-07-13
;  PRIOR APPLICATION NUMBER: EP 99202316.8
;  PRIOR FILING DATE: 1999-07-14
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 3260
;   TYPE: DNA
;   ORGANISM: Infectious bursal disease virus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(3260)
;   OTHER INFORMATION: Consensus cDNA sequence of IBDV A-segment
US-10-046-671B-70

  Query Match             17.4%;  Score 246;  DB 6;  Length 3260;
  Best Local Similarity   49.5%;  Pred. No. 8.9e-68;
  Matches  680;  Conservative   34;  Mismatches  639;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
Db        181 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTRGAGAAGCACAC 240

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
Db        241 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 300

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
Db        301 TGTCTTTTTCCCTGGWTTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 357

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
Db        358 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGYTA 417

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
Db        418 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTGAGGTCAAGCACACTYCCTGGTGG 477

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
Db        478 CGTTTATGCACTAAAYGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 537

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
Db        538 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATYGG 597

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
Db        598 GAACGTCCTAGTAGGGGAAGGGGTMACCGTCCTCAGCTTACCCACATCATATGATCTTGG 657

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
Db        658 GTATGTGAGRCTYGGTGACCCCATTCCCGCWATAGGGCTYGACCCAAAAATGGTAGCMAC 717

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
Db        718 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATGATTACCAATT 777

Qy        633 CCTACCCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
Db        778 CTCATCACAGTACCAASCAGGTGGGGTAACAATCACACTGTTCTCAGCYAAYATYGATGC 837

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
Db        838 CATCACAAGCCTCAGCRTYGGGGGAGARCTCGTGTTTCAAACAAGCGTCCAMGGCCTTRT 897

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
Db        898 ACTGGGYGCYACCATCTACCTYATAGGCTTTGATGGGACWGCGGTAATCACCAGRGCTGT 957

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
Db        958 GGCCGCARACAATGGGCTRACGRCCGGCACYGACAACCTTWTGCCATTCAATMTTGTGAT 1017

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
Db       1018 TCCAACMARCGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTC 1074

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
Db       1075 CAA----AAGTGGTGGTCAGGCRGGGGATCAGATGTCRTGGTCRGCAAGWGGGAGCC--- 1127

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
Db       1128 -----TAGCAGTGACGATCCAYGGTGGCAACTATCCAGGGGCCCTCCGTCCCGTCACRCT 1182

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
Db       1183 AGTRGCCTACGAAAGAGTGGCAACAGGATCYGTCGTTACGGTCGCYGGGGTGAGCAACTT 1242

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
Db       1243 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTYACAGAATACGGCCGATTTGA 1302

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
Db       1303 CCCAGGAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGTCTTGGCATCAA 1362

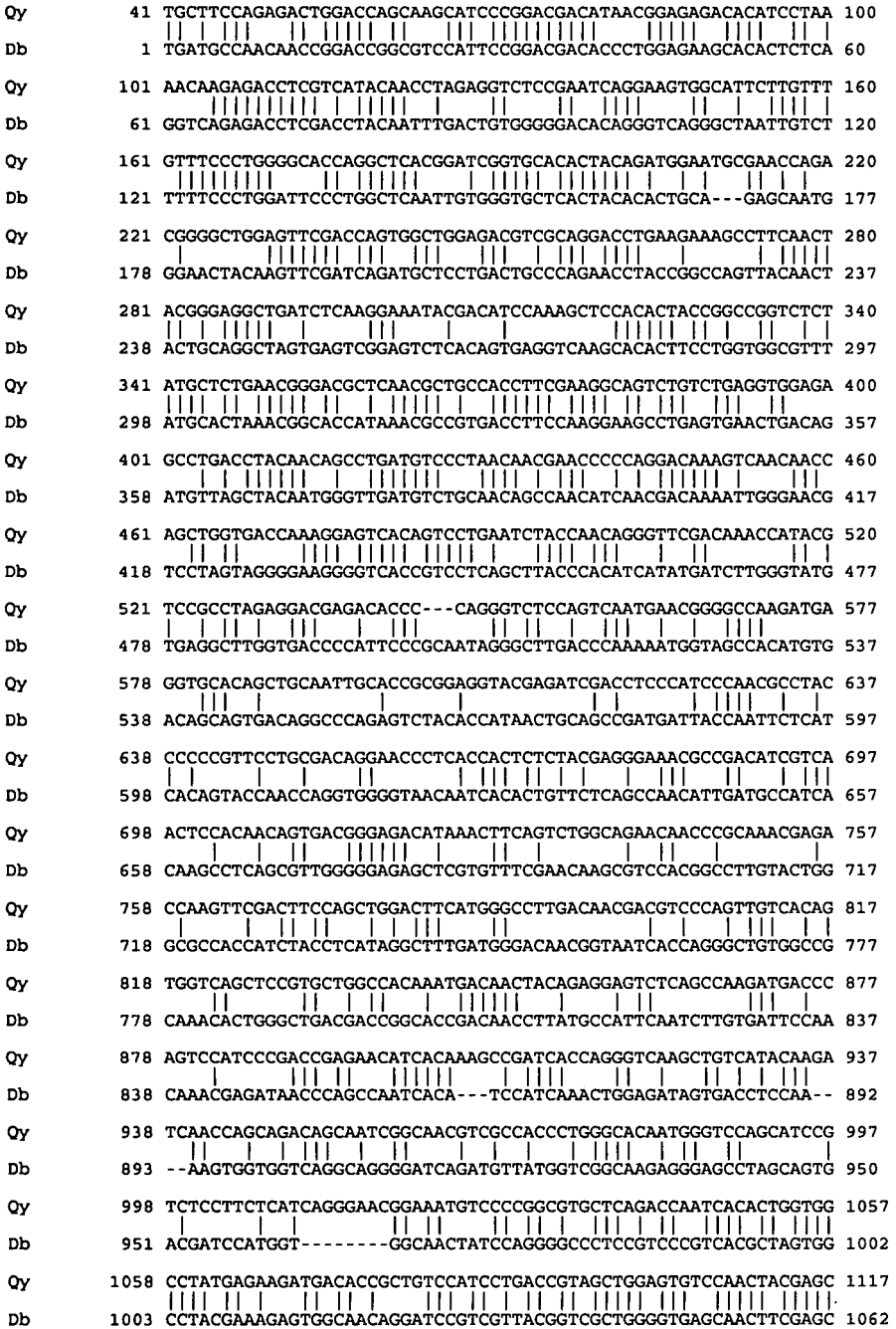
Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
Db       1363 GACCGTMTGGCCAACAAGGGAGTACACTGACTTTCGYGARTACTTCATGGAGGTGGCCGA 1422

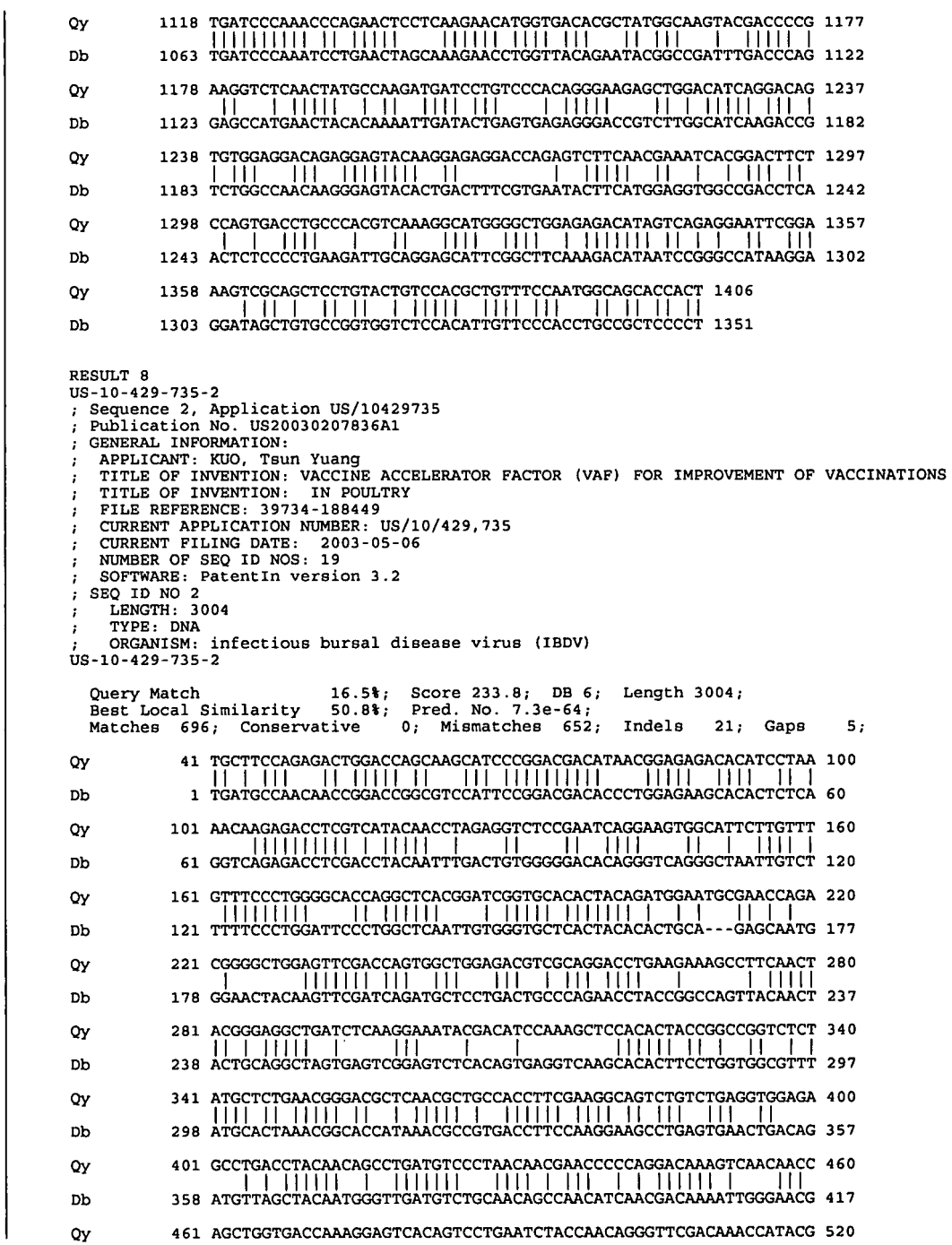
Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
Db       1423 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTYGGCTTCAAAGACATAATCCGGGCCMT 1482

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
Db       1483 AAGGAGGATAGCTGTGCCGGTGGTCTCYACAYTGTTCCCACCYGCCGCTCCCCT 1536

RESULT 7
US-10-377-718-2
; Sequence 2, Application US/10377718
; Publication No. US20030175291A1
; GENERAL INFORMATION:
;  APPLICANT: KUO, Tsun Yuang
;  TITLE OF INVENTION: MULTIPLE AND MULTIVALENT DNA VACCINES IN OVO
;  FILE REFERENCE: 39734-186920
;  CURRENT APPLICATION NUMBER: US/10/377,718
;  CURRENT FILING DATE:  2003-03-04
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 3004
;   TYPE: DNA
;   ORGANISM: infectious bursal disease virus (IBDV)
US-10-377-718-2

  Query Match             16.5%;  Score 233.8;  DB 6;  Length 3004;
  Best Local Similarity   50.8%;  Pred. No. 7.3e-64;
  Matches  696;  Conservative    0;  Mismatches  652;  Indels   21;  Gaps    5;
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RESULT 8
US-10-429-735-2
; Sequence 2, Application US/10429735
; Publication No. US20030207836A1
; GENERAL INFORMATION:
; APPLICANT: KUO, Tsun Yuang
; TITLE OF INVENTION: VACCINE ACCELERATOR FACTOR (VAF) FOR IMPROVEMENT OF VACCINATIONS
; TITLE OF INVENTION: IN POULTRY
; FILE REFERENCE: 39734-188449
; CURRENT APPLICATION NUMBER: US/10/429,735
; CURRENT FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: infectious bursal disease virus (IBDV)
US-10-429-735-2

Query Match 16.5%; Score 233.8; DB 6; Length 3004;
Best Local Similarity 50.8%; Pred. No. 7.3e-64;
Matches 696; Conservative 0; Mismatches 652; Indels 21; Gaps 5;

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Db        418 TCCTAGTAGGGGAAGGGGTCACCGTCCTCAGCTTACCCACATCATATGATCTTGGGTATG 477

Qy        521 TCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAAGATGA 577

Db        478 TGAGGCTTGGTGACCCCATTCCCGCAATAGGGCTTGACCCAAAAATGGTAGCCACATGTG 537

Qy        578 GGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACGCCTAC 637

Db        538 ACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATGATTACCAATTCTCAT 597

Qy        638 CCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACATCGTCA 697

Db        598 CACAGTACCAACCAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGCCATCA 657

Qy        698 ACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGA 757

Db        658 CAAGCCTCAGCGTTGGGGGAGAGCTCGTGTTTCGAACAAGCGTCCACGGCCTTGTACTGG 717

Qy        758 CCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAG 817

Db        718 GCGCCACCATCTACCTCATAGGCTTTGATGGGACAACGGTAATCACCAGGGCTGTGGCCG 777

Qy        818 TGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGATGACCC 877

Db        778 CAAACACTGGGCTGACGACCGGCACCGACAACCTTATGCCATTCAATCTTGTGATTCCAA 837

Qy        878 AGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGA 937

Db        838 CAAACGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTCCAA-- 892

Qy        938 TCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCG 997

Db        893 --AAGTGGTGGTCAGGCAGGGGATCAGATGTTATGGTCGGCAAGAGGGAGCCTAGCAGTG 950

Qy        998 TCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGG 1057

Db        951 ACGATCCATGGT--------GGCAACTATCCAGGGGCCCTCCGTCCCGTCACGCTAGTGG 1002

Qy       1058 CCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGC 1117

Db       1003 CCTACGAAAGAGTGGCAACAGGATCCGTCGTTACGGTCGCTGGGGTGAGCAACTTCGAGC 1062

Qy       1118 TGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGACCCCG 1177

Db       1063 TGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGACCCAG 1122

Qy       1178 AAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAG 1237

Db       1123 GAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGTCTTGGCATCAAGACCG 1182

Qy       1238 TGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCT 1297

Db       1183 TCTGGCCAACAAGGGAGTACACTGACTTTCGTGAATACTTCATGGAGGTGGCCGACCTCA 1242

Qy       1298 CCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGA 1357

Db       1243 ACTCTCCCCTGAAGATTGCAGGAGCATTCGGCTTCAAAGACATAATCCGGGCCATAAGGA 1302

Qy       1358 AAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406

Db       1303 GGATAGCTGTGCCGGTGGTCTCCACATTGTTCCCACCTGCCGCTCCCCT 1351


RESULT 9
US-10-046-671B-71
; Sequence 71, Application US/10046671B
; Publication No. US20030152592A1
; GENERAL INFORMATION:
;  APPLICANT: Boot, Hendrik J.
;  APPLICANT:  Huurne ter, Anna A.H.M
;  APPLICANT:  Peeters, Bernardus P.H.
;  TITLE OF INVENTION: Mosaic Infectious Bursal Disease Virus Vaccines
;  FILE REFERENCE: 2183-5238US
;  CURRENT APPLICATION NUMBER: US/10/046,671B
;  CURRENT FILING DATE:  2002-01-14
;  PRIOR APPLICATION NUMBER: PCT/NL00/00493
;  PRIOR FILING DATE: 2000-07-13
;  PRIOR APPLICATION NUMBER: EP 99202316.8
;  PRIOR FILING DATE: 1999-07-14
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
;   LENGTH: 3260
;   TYPE: DNA
;   ORGANISM: Infectious bursal disease virus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(3260)
;   OTHER INFORMATION: cDNA sequence CEF94-A of IBDV A-segment
US-10-046-671B-71

  Query Match             16.4%;  Score 232.4;  DB 6;  Length 3260;
  Best Local Similarity   50.7%;  Pred. No. 2.1e-63;
  Matches  697;  Conservative    0;  Mismatches  656;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95

Db        181 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 240

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155

Db        241 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 300

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215

Db        301 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 357

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275

Db        358 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGTTA 417

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335

Db        418 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTGAGGTCAAGCACACTTCCTGGTGG 477

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395

Db        478 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 537

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455

Db        538 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 597

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515

Db        598 GAACGTCCTAGTAGGGGAAGGGGTCACCGTCCTCAGCTTACCCACATCATATGATCTTGG 657

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572

Db        658 GTATGTGAGGCTTGGTGACCCCATTCCCGCAATAGGGCTTGACCCAAAAATGGTAGCCAC 717

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632

Db        718 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATGATTACCAATT 777

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692

Db        778 CTCATCACAGTACCAACCAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 837

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752

Db        838 CATCACAAGCCTCAGCGTTGGGGGAGAGCTCGTGTTTCAAACAAGCGTCCACGGCCTTGT 897

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
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Db        898 ACTGGGCGCCACCATCTACCTCATAGGCTTTGATGGGACAGCGGTAATCACCAGGGCTGT 957

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872

Db        958 GGCCGCAAACAATGGGCTGACGACCGGCACCGACAACCTTTTGCCATTCAATCTTGTGAT 1017

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932

Db       1018 TCCAACMARCGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTC 1074

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992

Db       1075 CAA----AAGTGGTGGTCAGGCAGGGGATCAGATGTCGTGGTCGGCAAGAGGGAGCCTAG 1130

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052

Db       1131 CAGTGACGATCCATGGT--------GGCAACTATCCAGGGGCCCTCCGTCCCGTCACGCT 1182

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112

Db       1183 AGTGGCCTACGAAAGAGTGGCAACAGGATCCGTCGTTACGGTCGCTGGGGTGAGCAACTT 1242

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172

Db       1243 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1302

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232

Db       1303 CCCAGGAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGTCTTGGCATCAA 1362

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292

Db       1363 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAATACTTCATGGAGGTGGCCGA 1422

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352

Db       1423 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTCGGCTTCAAAGACATAATCCGGGCCAT 1482

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406

Db       1483 AAGGAGGATAGCTGTGCCGGTGGTCTCCACATTGTTCCCACCTGCCGCTCCCCT 1536


RESULT 10
US-10-046-671B-72
; Sequence 72, Application US/10046671B
; Publication No. US20030152592A1
; GENERAL INFORMATION:
;  APPLICANT: Boot, Hendrik J.
;  APPLICANT:  Huurne ter, Anna A.H.M
;  APPLICANT:  Peeters, Bernardus P.H.
;  TITLE OF INVENTION: Mosaic Infectious Bursal Disease Virus Vaccines
;  FILE REFERENCE: 2183-5238US
;  CURRENT APPLICATION NUMBER: US/10/046,671B
;  CURRENT FILING DATE:  2002-01-14
;  PRIOR APPLICATION NUMBER: PCT/NL00/00493
;  PRIOR FILING DATE: 2000-07-13
;  PRIOR APPLICATION NUMBER: EP 99202316.8
;  PRIOR FILING DATE: 1999-07-14
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 3260
;   TYPE: DNA
;   ORGANISM: Infectious bursal disease virus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(3260)
;   OTHER INFORMATION: cDNA sequence D6948-A of IBDV A-segment
US-10-046-671B-72

  Query Match             16.4%;  Score 232;  DB 6;  Length 3260;
  Best Local Similarity   50.7%;  Pred. No. 2.9e-63;

  Matches  696;  Conservative    1;  Mismatches  656;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCCGGACGACATAACGGAGAGACACAT 95

Db        181 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTAGAGAAGCACAC 240

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155

Db        241 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 300

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215

Db        301 TGTCTTTTCCCTGGTTTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 357

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275

Db        358 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 417

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335

Db        418 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTGAGGTCAAGCACACTCCCTGGTGG 477

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395

Db        478 CGTTTATGCACTAAATGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 537

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455

Db        538 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATCGG 597

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515

Db        598 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATCTTGG 657

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572

Db        658 GTATGTGAGACTCGGTGACCCCATTCCCGCTATAGGGCTCGACCCAAAAATGGTAGCAAC 717

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632

Db        718 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATGATTACCAATT 777

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692

Db        778 CTCATCACAGTACCAAGCAGGTGGGGTAACAATCACACTGTTCTCAGCTAATATCGATGC 837

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752

Db        838 CATCACAAGCCTCAGCATCGGGGGAGAACTCGTGTTTCAAACAAGCGTCCAAGGCCTTAT 897

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812

Db        898 ACTGGGTGCTACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 957

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872

Db        958 GGCCGCARACAATGGGCTAACGGCCGGCACTGACAACCTTATGCCATTCAATATTGTGAT 1017

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932

Db       1018 TCCAACCAGCGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTC 1074

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992

Db       1075 CAA----AAGTGGTGGTCAGGCGGGGGATCAGATGTCATGGTCAGCAAGTGGGAGCC--- 1127

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052

Db       1128 -----TAGCAGTGACGATCCACGGTGGCAACTATCCAGGGGCCCTCCGTCCCGTCACACT 1182

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112

Db       1183 AGTAGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCCGGGGTGAGCAACTT 1242
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Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
              |||||||||||||||| || |||||    |||||| |||| |||    || |||    | ||
Db       1243 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTCACAGAATACGGCCGATTTGA 1302

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
              ||| | ||   | |||||  | ||  |||| |||     | |||||    || | |||||
Db       1303 CCCAGGAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGTCTTGGCATCAA 1362

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
              ||| || |||   |||  |||||||| ||      |    |||||  ||  |  | ||
Db       1363 GACCGTATGGCCAACAAGGGAGTACACTGACTTTCGCGAGTACTTCATGGAGGTGGCCGA 1422

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
              | ||  |  |  |||| |   ||  |||| |||| | ||||||| || | |   |
Db       1423 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCCT 1482

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
                 |||  | || |  || ||  | || || ||||| |||   || || || ||
Db       1483 AAGGAGGATAGCTGTGCCGGTGGTCTCTACACTGTTCCCACCCGCCGCTCCCCT 1536


RESULT 11
US-09-964-895-1
; Sequence 1, Application US/09964895
; Publication No. US20030099667A1
; GENERAL INFORMATION:
;  APPLICANT: Zeon Corporation
;  TITLE OF INVENTION: Avian herpesvirus-based recombinant Gumboro disease
;  TITLE OF INVENTION:  vaccine
;  FILE REFERENCE: rHVT/IBD-E
;  CURRENT APPLICATION NUMBER: US/09/964,895
;  CURRENT FILING DATE:  2001-09-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1374
;   TYPE: DNA
;   ORGANISM: Infectious bursal disease virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1368)
;   OTHER INFORMATION: product: VP2 of IBDV E strain
US-09-964-895-1

  Query Match             15.8%;  Score 223.4;  DB 3;  Length 1374;
  Best Local Similarity   50.8%;  Pred. No. 1.2e-60;
  Matches  673;  Conservative    0;  Mismatches  631;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
              | |  || | |||   || ||||| ||   ||| ||||||||||    |||||  ||||
Db         57 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 116

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
               || |   |||||||||| | |||||  |   ||   ||  ||||   ||  |  |
Db        117 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 176

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
              ||| | |||||||||     || ||||||     | ||||| |||||||  |  | |   ||
Db        177 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 233

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
              | |   |       |||||| |||  |||   |||  | ||| ||||    |      ||
Db        234 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 293

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
              ||||||| | |||||  |     |||    |   |              ||||| || |  ||
Db        294 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 353

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
               | ||||| || ||||| ||  | |||||  |  ||||||  |||| || |||  ||  |
Db        354 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 413

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
              |     | | |||||||  |  |||||||   ||||  | |||  | |  ||||||  |
Db        414 GACAGATGTTAGCTACAACGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 473

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
              |||   || ||     |||| || || ||||| |   |||| |||    |  ||
Db        474 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATCTTGG 533

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
              || ||  | || |  |||   | ||||     || ||   |  |||  |  |  || |
Db        534 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 593

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
                    |||  |          |          |          | |      | ||||
Db        594 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATAATTACCAATT 653

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              |  | | |       |   |    ||         | ||| || | |   |  |||   ||
Db        654 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 713

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
              | |||       |  ||  ||||||  |   ||||       |  |||  |
Db        714 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAACAAGCGTCCAAAGCCTTGT 773

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
              |  |      |  || ||  |  | |||    ||   ||       |  |  || |||
Db        774 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 833

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
              | |   ||      ||  ||||   | |||||     |    | ||         |||
Db        834 GGCCGCAAACAATGGGCTGACGGCCGGCATCGACAATCTTATGCCATTCAATCTTGTGAT 893

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
              |    |||  ||  ||||||    | ||||    ||  |   || | |
Db        894 TCCAACCAATGAGATAACCCAGCCAATCACAT---CCATCAAACTGGAGATAGTGACCTC 950

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
              ||| |   |   ||| |||     || |  |  | ||   | ||||    ||  ||
Db        951 CAAAAGTGATGGTCAGGCAG----GGGAACAGATGTCATGGTCGGCAAGTGGGAGCC--- 1003

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
                  |  |  |  |          || ||    || || |  ||| | ||  |||||||
Db       1004 -----TAGCAGTGACGATCCATGGTGGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1058

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
              |||||||  || |   || || |   ||  || | || || ||||| |||  |||||
Db       1059 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1118

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
              |||||||||||||||| || |||||    |||||| |||| |||    || |||    | ||
Db       1119 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1178

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
              ||| | ||   | |||||  | ||  |||| |||     | |||||    || | |||||
Db       1179 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCGCCTTGGCATCAA 1238

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
              ||| || |||   |||  |||||||| ||                |||||  ||  |  | ||
Db       1239 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1298

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
              | ||  |  |  |||| |   ||  |||| |||| | ||||||| || | |   ||
Db       1299 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1358

Qy       1353 TCGGA 1357
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Db       1359 AAGGA 1363


RESULT 12
US-10-832-353-1
; Sequence 1, Application US/10832353
; Publication No. US20040197351A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Zeon Corporation
;  TITLE OF INVENTION: Avian herpesvirus-based recombinant Gumboro disease
;  TITLE OF INVENTION:  vaccine
;  FILE REFERENCE: rHVT/IBD-E
;  CURRENT APPLICATION NUMBER: US/10/832,353
;  CURRENT FILING DATE:  2004-04-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1374
;   TYPE: DNA
;   ORGANISM: Infectious bursal disease virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1368)
;   OTHER INFORMATION: product: VP2 of IBDV E strain
US-10-832-353-1

  Query Match            15.8%;  Score 223.4;  DB 8;  Length 1374;
  Best Local Similarity   50.8%;  Pred. No. 1.2e-60;
  Matches  673;  Conservative    0;  Mismatches  631;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
              | |  || | |||   || ||||| ||   ||| ||||||||||    |||||  ||||
Db         57 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 116

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
              || |    |||||||||| | |||||  |    ||    ||  ||||    || |  |
Db        117 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 176

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
              ||| | |||||||||    || ||||||    | ||||| ||||||| |  | |   ||
Db        177 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 233

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
              | |   |       |||||||| |||  |||   |||  | ||| ||||    |      ||
Db        234 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 293

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
              |||||||  | |||||  |      |||    |    |           |||||| || |  ||
Db        294 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 353

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
                | ||||| || ||||| ||  | |||||  |  |||||| |||| || |||  |||  |
Db        354 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 413

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
              |       | | |||||||  |  ||||||||    |||| | |||  | | ||||||  |
Db        414 GACAGATGTTAGCTACAACGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 473

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
              |||   || ||     |||| || || ||||| |   |||| |||    |  ||
Db        474 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATCTTGG 533

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
              || ||  | || |  |||   | ||||      || ||  |  |||  |  |  || |
Db        534 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 593

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
                  |||  |           |      |           | |      | ||||
Db        594 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATAATTACCAATT 653

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              | | | |     |   |    ||       | ||| || | |   |  |||   ||
Db        654 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 713

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
              | |||       |  ||   ||||||  |    ||||        |  |||  |
Db        714 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAACAAGCGTCCAAAGCCTTGT 773

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
                | |     |  || ||   | | |||    ||   ||       |  |  || |||

Db        774 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 833

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
                | |    ||       ||  ||||   |  |||||    |    | ||        |||
Db        834 GGCCGCAAACAATGGGCTGACGGCCGGCATCGACAATCTTATGCCATTCAATCTTGTGAT 893

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
              |              ||| ||   ||||||    | ||||    ||  |   || | |
Db        894 TCCAACCAATGAGATAACCCAGCCAATCACAT---CCATCAAACTGGAGATAGTGACCTC 950

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
              ||| |   |    ||| |||      || |  |  | ||   | ||||    ||  ||
Db        951 CAAAAGTGATGGTCAGGCAG----GGGAACAGATGTCATGGTCGGCAAGTGGGAGCC--- 1003

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
                  |  |  |  |          || ||    || || |  ||| | ||  ||||||
Db       1004 -----TAGCAGTGACGATCCATGGTGGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1058

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
              |||||||| || |   || || |    ||  || | || || ||||| |||  |||||
Db       1059 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1118

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
              |||||||||||||| || |||||    ||||| |||    || |||    | ||
Db       1119 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1178

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
              ||| | ||   | |||||  | ||  |||| |||    | |||||    || | |||||
Db       1179 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCGCCTTGGCATCAA 1238

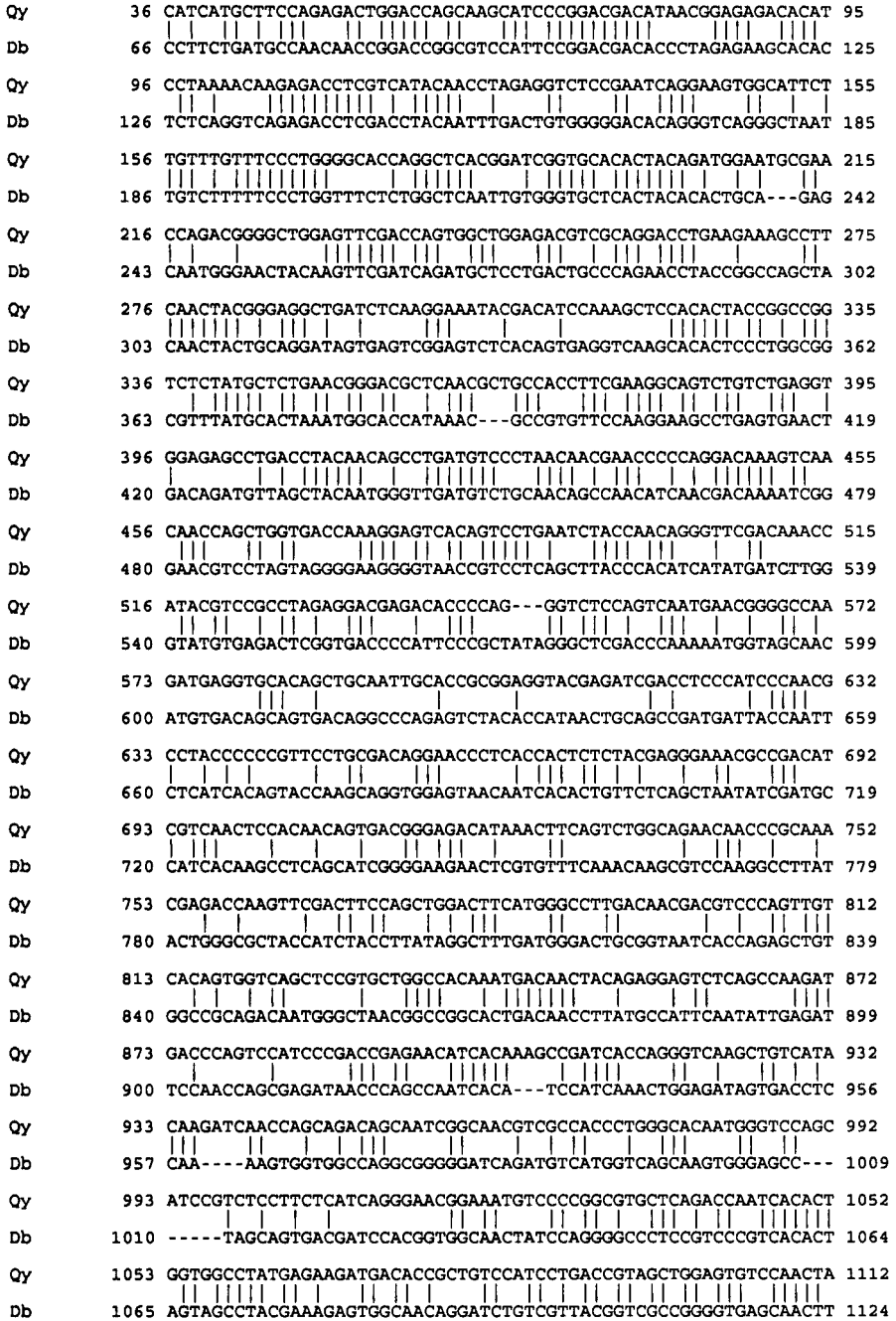
Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
              ||| || |||   |||  |||||||| ||             |||||  ||  |  | ||
Db       1239 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1298

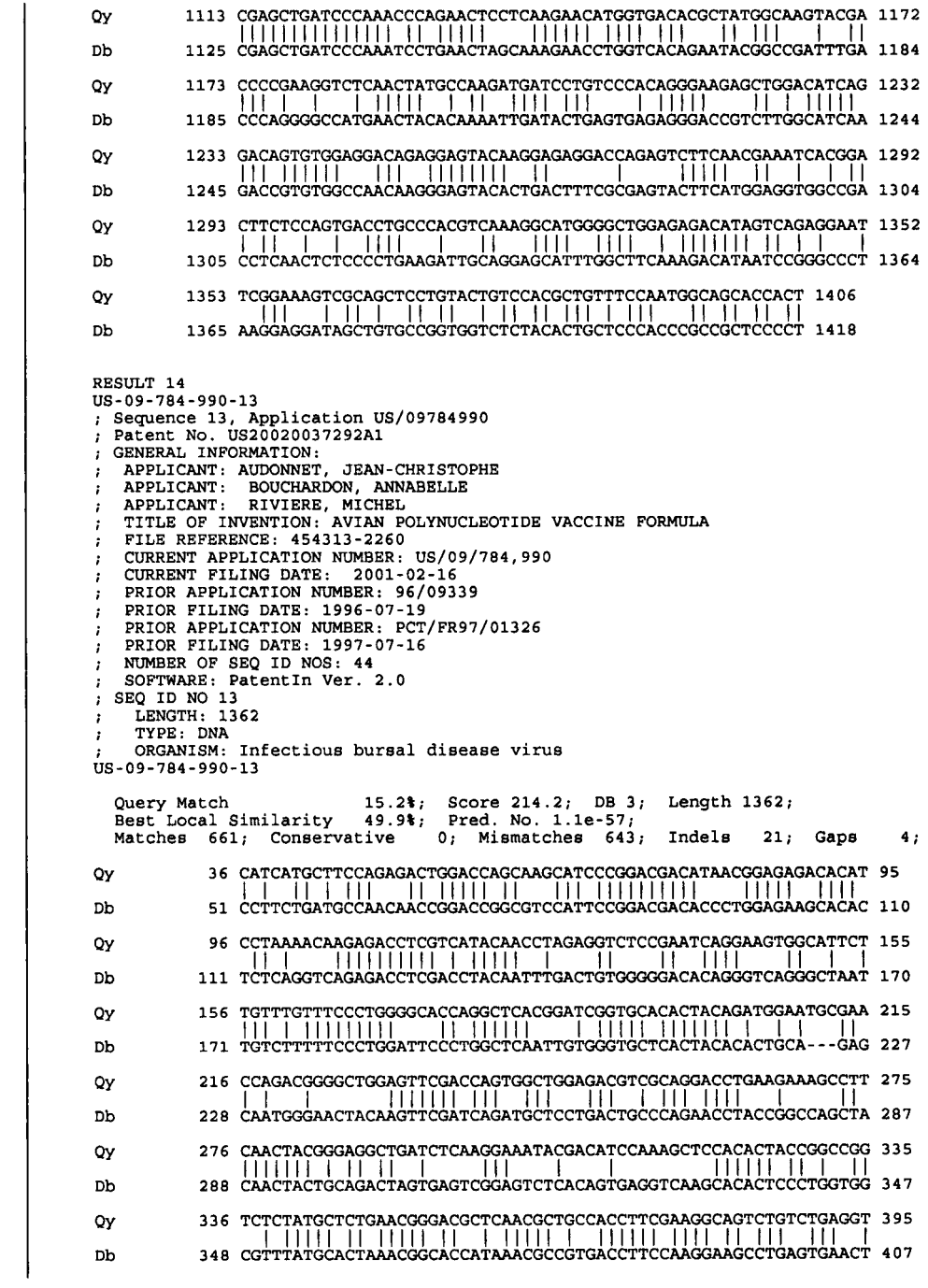
Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
              | ||  |  | ||||  |  ||  ||||  ||||  | |||||| || | |  ||
Db       1299 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1358

Qy       1353 TCGGA 1357
                |||
Db       1359 AAGGA 1363


RESULT 13
US-09-477-574A-1
; Sequence 1, Application US/09477574A
; Publication No. US20020015708A1
; GENERAL INFORMATION:
;  APPLICANT: Stram, Yehuda
;  APPLICANT:  Rogel, Arie
;  APPLICANT:  Sela, Ilan
;  APPLICANT:  Edelbaum, Orit
;  APPLICANT:  Shachar, Yehoshua
;  APPLICANT:  Zanberg, Yehuda
;  APPLICANT:  Gontmakher, Tanya
;  APPLICANT:  Khayat, Eli
;  TITLE OF INVENTION: RECOMBINANT VACCINES AGAINST IBDV
;  FILE REFERENCE: 0231.00013
;  CURRENT APPLICATION NUMBER: US/09/477,574A
;  CURRENT FILING DATE:  2000-01-04
;  PRIOR APPLICATION NUMBER: 60/114,634
;  PRIOR FILING DATE: 1999-01-04
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 3054
;   TYPE: DNA
;   ORGANISM: Infectious bursal disease virus
US-09-477-574A-1

  Query Match            15.3%;  Score 216.4;  DB 3;  Length 3054;
  Best Local Similarity   50.5%;  Pred. No. 3e-58;
  Matches  694;  Conservative    0;  Mismatches  656;  Indels   24;  Gaps    6;
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RESULT 14
US-09-784-990-13
; Sequence 13, Application US/09784990
; Patent No. US20020037292A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/09/784,990
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Infectious bursal disease virus
US-09-784-990-13

Query Match 15.2%; Score 214.2; DB 3; Length 1362;
Best Local Similarity 49.9%; Pred. No. 1.1e-57;
Matches 661; Conservative 0; Mismatches 643; Indels 21; Gaps 4;

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Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
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Db        408 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 467

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
               ||    |||||      |||| |||||  |||||  |   |||||  |||    |   ||
Db        468 GAATGTCCTGGTAGGGGAAGGGGTCACTGTCCTCAGCCTACCCACATCATATGATCTTGG 527

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
               || ||  | || |  |||   |  |||     || ||  |  |||  |  |  || |
Db        528 GTATGTGAGGCTTGGTGACCCCATTCCCGCTATAGGGCTTGACCCAAAAATGGTAGCTAC 587

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
                  |||  |          |       |            | |       | ||||
Db        588 ATGCGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATGATTACCAATT 647

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              |  | | |      |   |    ||       | ||| || | |   |  |||   ||
Db        648 CTCATCACAGTACCAACCAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 707

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
               |||    |   |   |  ||||||  |    ||          |  |||  |
Db        708 TATCACAAGCCTCAGCATTGGGGGAGAGCTCGTGTTTCAAACAAGCGTCCAAGGCCTTGT 767

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
                | |      |  || ||   | | |||    ||   ||        |  |  || |||
Db        768 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 827

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
               | |  |  |      ||  ||||   |  |||||     |    | ||
Db        828 AGCCGCAGATAATGGGCTGACGGCCGGCACCGACAATCTTATGCCATTC---------- 876

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
               |  |    ||| || ||| |  | || ||  |||| |||||     |||| |||    |
Db        877 -AATCTTGTCATTCCAACCAATGAGATAACCCAGCCAATCACATCCATCAAACTG---GA 932

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
               |   | | |    | |  |          |  |       ||        ||     |
Db        933 GATAGTGACCTCCAAAAGTGGTGGTCAGGCAGGGGATCAGATGTCATGGTCGGCAAGTGG 992

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
               |  |  |  |  |      || ||    || ||  |  ||| |  ||  |||||||
Db        993 GAGCCTAGCAGTGACGATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCCGTCACACT 1052

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
              || ||||| || |   || || |    ||| || | || || |||||  |||   ||||
Db       1053 AGTAGCCTACGAAAGAGTGGCAACAGGATCCGTCGTTACGGTCGCTGGGGTGAGTAACTT 1112

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
              |||||||||  |||||  || |||||    |||||| |||| |||   || |||   |  ||
Db       1113 CGAGCTGATTCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1172

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
              |||  |  ||   | |||||  |  ||  |||| |||    | |||||    || | |||||
Db       1173 CCCAGGAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGTCTTGGCATCAA 1232

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
              |||  ||  |||   |||  ||||||||  ||          |||||  ||  |  | ||
Db       1233 GACCGTCTGGCCAACAAGGGAGTACACTGATTTTCGTGAGTACTTCATGGAGGTGGCCGA 1292

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
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Db       1293 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCTAT 1352

Qy       1353 TCGGA 1357
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Db       1353 AAGGA 1357


RESULT 15
US-10-229-412-13
; Sequence 13, Application US/10229412
; Publication No. US20030124145A1
; GENERAL INFORMATION:
;  APPLICANT: AUDONNET, JEAN-CHRISTOPHE
;  APPLICANT:  BOUCHARDON, ANNABELLE
;  APPLICANT:  RIVIERE, MICHEL
;  TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
;  FILE REFERENCE: 454313-2260
;  CURRENT APPLICATION NUMBER: US/10/229,412
;  CURRENT FILING DATE:  2002-08-28
;  PRIOR APPLICATION NUMBER: US/09/232,479
;  PRIOR FILING DATE: 1999-01-15
;  PRIOR APPLICATION NUMBER: 96/09339
;  PRIOR FILING DATE: 1996-07-19
;  PRIOR APPLICATION NUMBER: PCT/FR97/01326
;  PRIOR FILING DATE: 1997-07-16
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 1362
;   TYPE: DNA
;   ORGANISM: Infectious bursal disease virus
US-10-229-412-13

  Query Match            15.2%;  Score 214.2;  DB 6;  Length 1362;
  Best Local Similarity   49.9%;  Pred. No. 1.1e-57;
  Matches  661;  Conservative    0;  Mismatches  643;  Indels   21;  Gaps    4;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
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Db         51 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 110

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
               ||  |    |||||||||| | |||||  |    ||     ||  ||||    ||  | |
Db        111 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 170

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
              ||| | ||||||||||     || ||||||     | |||||  |||||||  |  | |   ||
Db        171 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 227

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
              | |   |       |||||| |||  |||   |||  | ||| ||||    |      ||
Db        228 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 287

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
              ||||||| | || ||  |     |||    |    |        ||||||  || |  ||
Db        288 CAACTACTGCAGACTAGTGAGTCGGAGTCTCACAGTGAGGTCAAGCACACTCCCTGGTGG 347

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
              | |||||  || |||||  ||  | |||||  |  ||||||  ||||  ||  |||  |||  |
Db        348 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 407

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
              |       | | ||||||  |  |||||||   ||||  | |||  | | ||||||  |
Db        408 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 467

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
               ||    |||||      |||| |||||  |||||  |   |||||  |||    |   ||
Db        468 GAATGTCCTGGTAGGGGAAGGGGTCACTGTCCTCAGCCTACCCACATCATATGATCTTGG 527

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
               || ||  | || |  |||   |  |||     || ||  |  |||  |  |  || |
Db        528 GTATGTGAGGCTTGGTGACCCCATTCCCGCTATAGGGCTTGACCCAAAAATGGTAGCTAC 587

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
                  |||  |          |       |            | |       | ||||
Db        588 ATGCGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATGATTACCAATT 647

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              |  | | |      |   |    ||       | ||| || | |   |  |||   ||
Db        648 CTCATCACAGTACCAACCAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 707

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
               |||    |   |   |  ||||||  |    ||          |  |||  |
Db        708 TATCACAAGCCTCAGCATTGGGGGAGAGCTCGTGTTTCAAACAAGCGTCCAAGGCCTTGT 767
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Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
Db        768 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 827

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
Db        828 AGCCGCAGATAATGGGCTGACGGCCGGCACCGACAATCTTATGCCATTC---------- 876

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
Db        877 -AATCTTGTCATTCCAACCAATGAGATAACCCAGCCAATCACATCCATCAAACTG---GA 932

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
Db        933 GATAGTGACCTCCAAAAGTGGTGGTCAGGCAGGGGATCAGATGTCATGGTCGGCAAGTGG 992

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
Db        993 GAGCCTAGCAGTGACGATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCCGTCACACT 1052

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
Db       1053 AGTAGCCTACGAAAGAGTGGCAACAGGATCCGTCGTTACGGTCGCTGGGGTGAGTAACTT 1112

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
Db       1113 CGAGCTGATTCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1172

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
Db       1173 CCCAGGAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGTCTTGGCATCAA 1232

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
Db       1233 GACCGTCTGGCCAACAAGGGAGTACACTGATTTTCGTGAGTACTTCATGGAGGTGGCCGA 1292

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
Db       1293 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCTAT 1352

Qy       1353 TCGGA 1357
Db       1353 AAGGA 1357
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 14:33:26 ; Search time 330 Seconds
(without alignments)
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Perfect score: 1413
Sequence: 1 aacaccaacaaggcaaccgc.....tggcagcaccactcatcgga 1413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6068529 seqs, 419036697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
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11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	37	2.6	8280	8	US-11-000-688-641	Sequence 641, App
	2	36.4	2.6	900	7	US-10-821-234-61	Sequence 61, Appl
	3	36.2	2.6	6328	8	US-11-136-527-3049	Sequence 3049, Ap
	4	36	2.5	7127	8	US-11-090-439-41	Sequence 41, Appl
	5	35.6	2.5	200628	8	US-11-121-086-62	Sequence 62, Appl
	6	35	2.5	2279	7	US-10-509-121-37	Sequence 37, Appl
	7	35	2.5	2301	7	US-10-509-121-1	Sequence 1, Appli
	8	35	2.5	2301	7	US-10-509-121-38	Sequence 38, Appl
	9	34	2.4	3564	7	US-10-601-368-20	Sequence 20, Appl
	10	34	2.4	4858	7	US-10-601-368-19	Sequence 19, Appl
	11	33.4	2.4	2294	7	US-10-509-121-5	Sequence 5, Appli
	12	33.4	2.4	2294	7	US-10-509-121-7	Sequence 7, Appli
	13	33.4	2.4	2300	7	US-10-509-121-3	Sequence 3, Appli
	14	33	2.3	2295	6	US-10-649-457-1	Sequence 1, Appli
c	15	33	2.3	98309	8	US-11-124-368A-2921	Sequence 2921, Ap
	16	32.8	2.3	765	7	US-10-467-657-2425	Sequence 2425, Ap
c	17	32.4	2.3	4403	8	US-11-136-527-2391	Sequence 2391, Ap
	18	32.4	2.3	6189	6	US-10-877-346-10	Sequence 10, Appl
	19	32.4	2.3	6201	6	US-10-877-346-8	Sequence 8, Appli
c	20	32.2	2.3	835	7	US-10-750-185-50468	Sequence 50468, A
c	21	32.2	2.3	835	7	US-10-750-623-50468	Sequence 50468, A
c	22	32.2	2.3	928	7	US-10-750-185-36782	Sequence 36782, A
c	23	32.2	2.3	928	7	US-10-750-623-36782	Sequence 36782, A
	24	32.2	2.3	2211	8	US-11-136-527-3331	Sequence 3331, Ap
	25	32	2.3	1044	8	US-11-221-203-27	Sequence 27, Appl
	26	32	2.3	1050	8	US-11-221-203-25	Sequence 25, Appl
	27	32	2.3	2249	8	US-11-136-527-2388	Sequence 2388, Ap
c	28	32	2.3	2699	8	US-11-127-877-5	Sequence 5, Appli
c	29	32	2.3	394468	7	US-10-995-561-13473	Sequence 13473, A
c	30	31.8	2.3	3258	7	US-10-750-185-30056	Sequence 30056, A
c	31	31.8	2.3	3258	7	US-10-750-623-30056	Sequence 30056, A
	32	31.8	2.3	5247	7	US-10-750-185-64326	Sequence 64326, A
	33	31.8	2.3	5247	7	US-10-750-623-64326	Sequence 64326, A
c	34	31.8	2.3	110847	8	US-11-121-086-11	Sequence 11, Appl
	35	31.6	2.2	1587	6	US-10-897-981-11	Sequence 11, Appl
	36	31.6	2.2	2403	6	US-10-649-457-4	Sequence 4, Appli
c	37	31.6	2.2	2590	6	US-10-897-981-3	Sequence 3, Appli
	38	31.6	2.2	2736	7	US-10-858-730-38	Sequence 38, Appl
	39	31.6	2.2	2838	7	US-10-770-726-27	Sequence 27, Appl
c	40	31.4	2.2	1400	8	US-11-136-527-5138	Sequence 5138, Ap
c	41	31.4	2.2	2680	8	US-11-136-527-1042	Sequence 1042, Ap
	42	31.4	2.2	3187	7	US-10-947-249-189	Sequence 189, App
	43	31.4	2.2	3624	6	US-10-755-092-6	Sequence 6, Appli
	44	31.4	2.2	5093	8	US-11-136-527-2431	Sequence 2431, Ap
c	45	31.4	2.2	159146	8	US-11-121-086-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-11-000-688-641
; Sequence 641, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 641
; LENGTH: 8280
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(8280)
; OTHER INFORMATION: ankyrin 1, erythrocytic(ANK1) gene.
US-11-000-688-641

Query Match 2.6%; Score 37; DB 8; Length 8280;
Best Local Similarity 46.1%; Pred. No. 2.1;
Matches 124; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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Qy        533 ACGAGACACCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAA 592
              ||  | |  ||||||    |||  ||  ||  | |||   | ||   |  | |   || |
Db       2003 ACCTGGCCGCCCAGGAGGGCCACGCAGAGATGGTGGCTCTGCTGCTCTCGAAACAAGCCA 2062

Qy        593 TTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGA 652
               ||      | | || || ||| ||  ||| |  |||  |  ||      |       |
Db       2063 ATGGCAACCTGGGGAACAAGAGCGGACTCACTCCCCTCCATCTGGTAGCACAAGAAGGCC 2122

Qy        653 CAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGA 712
                |   |  |   |  ||          | |||  | |||  ||  || ||||  ||   ||
Db       2123 ACGTTCCAGTGGCAGATGTGCTGATCAAACACGGTGTCATGGTGGACGCCACCACCCGGA 2182

Qy        713 CGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCC 772
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Db       2183 TGGGCTACACTCCCCTCCATGTGGCCAGTCACTATGGAAACATCAAGCTGGTGAAGTTTC 2242

Qy        773 AGCTGGACTTCATGGGCCTTGACAACGAC 801
              |||| |   |  ||   || ||| | |
Db       2243 TGCTGCAGCACCAGGCAGATGTCAATGCC 2271


RESULT 2
US-10-821-234-61
; Sequence 61, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 61
;   LENGTH: 900
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-61

  Query Match             2.6%;  Score 36.4;  DB 7;  Length 900;
  Best Local Similarity   49.0%;  Pred. No. 0.9;
  Matches   97;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy       1144 AACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATGATC 1203
              ||||| | | |    |   |    | |||||  |||  ||    ||  | | |   ||
Db        204 AACATCATTAAATCACAACTCCTAAAAGACCCGCAAGTGCTATTTGCTGGCTACAAAGTC 263

Qy       1204 CTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAGGAG 1263
              |    || |  |||  |   | |||||    ||||  ||  ||   ||| ||||
Db        264 CCCCACCCCTTGGAGCACAAGATCATCATCCGAGTGCAGACCACGCCGGACTACAGCCCC 323

Qy       1264 AGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAGGCA 1323
                |        |   |||||  ||||| ||| ||  ||||||  ||| ||  |    |||
Db        324 CAGGAAGCCTTTACCAACGCCATCACCGACCTCATCAGTGAGCTGTCCCTGCTGGAGGAG 383

Qy       1324 TGGGGCTGGAGAGACATA 1341
              |   ||  | ||||
Db        384 CGCTTTCGGGTGGCCATA 401


RESULT 3
US-11-136-527-3049
; Sequence 3049, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3049
;   LENGTH: 6328
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-3049

  Query Match             2.6%;  Score 36.2;  DB 8;  Length 6328;
  Best Local Similarity   51.6%;  Pred. No. 3.2;
  Matches   83;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       1131 AGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTA 1190
              || || ||| ||| | | ||      | |||||   |   |   |   |       |||  |
Db       1793 AGTACACCTGAAGCAGAAGGAACAGCACTATGAGGAAAAGATCAAAGTGTTGGACAATCA 1852

Qy       1191 TGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGA 1250
                |||| |  | || || ||| |||     || || | || ||    | ||      |||
Db       1853 GATAAAGAAGGACTTGGCCGACAAGGAGAGCCTAGAGACCATGATGCAGAGGCACGAAGA 1912

Qy       1251 GGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGG 1291
              ||||  | | |||| |  ||   || ||| |||    | ||
Db       1913 GGAGGCCCACGAGAAGGGCAAGATCCTCAGCGAGCAGAAGG 1953


RESULT 4
US-11-090-439-41
; Sequence 41, Application US/11090439
; Publication No. US20050266442A1
; GENERAL INFORMATION:
;  APPLICANT: Squillace, Rachel
;  APPLICANT:  Weiner, Michael P.
;  TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
;  TITLE OF INVENTION:  Angiomyolipoma Cell and Method of Use Thereof
;  FILE REFERENCE: 24318-502
;  CURRENT APPLICATION NUMBER: US/11/090,439
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: 60/556,344
;  PRIOR FILING DATE: 2004-03-25
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 7127
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-090-439-41

  Query Match             2.5%;  Score 36;  DB 8;  Length 7127;
  Best Local Similarity   51.9%;  Pred. No. 3.9;
  Matches   81;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1138 CTCAAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAG 1197
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Db       3768 CTCAAGTACCTGGGGTGCCGCTACAGCGAGATCAAACCCTACGGACTTGACTGGGCGGAG 3827

Qy       1198 ATGATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTAC 1257
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Db       3828 CTCAGCCGGGACCTCAGGAAGACGTGTGAGGAGCAGACCCTGAGTATCCCCTACAACGAC 3887

Qy       1258 AAGGAGAGGACCAGAGTCTTCAACGAAATCACGGAC 1293
              | | |   | || ||   || |  |     | || |
Db       3888 TATGGGGACAGCAAAGAGATCTAGCACCATAAGGCC 3923


RESULT 5
US-11-121-086-62
; Sequence 62, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
;  APPLICANT: POULSEN, TIM S.
;  APPLICANT:  NIELSEN, KIRSTEN V.
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;  FILE REFERENCE: 09138.6000-00000
;  CURRENT APPLICATION NUMBER: US/11/121,086
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,570
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
;   LENGTH: 200628
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-62

  Query Match             2.5%;  Score 35.6;  DB 8;  Length 200628;
  Best Local Similarity   42.0%;  Pred. No. 36;
  Matches  206;  Conservative    0;  Mismatches  284;  Indels    0;  Gaps    0;

Qy        658 ACCCTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGA 717
              | | ||||||     |  |       | |  |  |||| ||| | |||| ||    |  |
Db     129462 ATCATCACCATCACCACCACCATCATCATCATCATCATCACCACCACTACCACCATCGTC 129521

Qy        718 GACATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTG 777
              ||| | | |||     |         |  | | |   ||||   ||  | ||
Db     129522 ACCATCATCATCATCACTGTCATCACCACTACCACCAGCACCATCATCATCGTCACCACC 129581

Qy        778 GACTTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCC 837
              |  |||   | |   || |  | ||       |||  |  ||| |  |   |  ||
Db     129582 ACCACCATCATCATCATCATCACCATCATCACCACCACCATCATCATCATCACCATCACC 129641

Qy        838 ACAAATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAAC 897
              || |    || |  ||       | |   ||  || |||     ||||   || |  |||
Db     129642 ACCACCATCATCATCATCACCACCACCATCATCATCACCATCATCATCATCACTGTCAAC 129701

Qy        898 ATCACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATC 957
              | |||  |   | | |||||   |||   |  |   ||  | || |      |     | |
Db     129702 ACCACTACCACCAGCACCATCATCATCGTCACCACCACCACCATCATCATCATCATCACC 129761

Qy        958 GGCAACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAAC 1017
              || |  | ||| | |   ||| ||     |  |   | ||  | || |  |     | |
Db     129762 ATCACCACCACCATCATCATCACCATCACCACCACCATCATCATCGTCACCACCACCACC 129821

Qy       1018 GGAAATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCG 1077
              | | |   | | |     |  | | |||      |  | |    |  || ||  |
Db     129822 ATCATTATTGTCATCATCACAATCACCACCACCACCATCATCAACACCATCATCACCACC 129881

Qy       1078 CTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTC 1137
              |   ||| | | | |  |||   |  | | || |    | |||   | |   |   ||
Db     129882 ATCATTATCATCATCATCACTGTCATCACTACCTCCATCATCATCATCATCATTGTCATC 129941

Qy       1138 CTCAAGAACA 1147
              ||  | ||
Db     129942 ACCATCACCA 129951


RESULT 6
US-10-509-121-37
; Sequence 37, Application US/10509121
; Publication No. US20050283855A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU, et al.
;  TITLE OF INVENTION: GENE CODING FOR ACETOLACTATE SYNTHASE
;  FILE REFERENCE: 1254-0259PUS1
;  CURRENT APPLICATION NUMBER: US/10/509,121
;  CURRENT FILING DATE:  2004-09-28
;  PRIOR APPLICATION NUMBER: JP 2002-95721
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;   LENGTH: 2279
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-10-509-121-37

  Query Match             2.5%;  Score 35;  DB 7;  Length 2279;
  Best Local Similarity   49.2%;  Pred. No. 4.1;
  Matches   92;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        798 CGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGG 857
              || |  |   |  |||   || | || |||||  |  |   |||   ||  |      |
Db        427 CGGCCGCGTCGGGGTCTGCGTCGCCACCTCCGGCCCCGGGGCAACCAACCTCGTGTCCGC 486

Qy        858 AGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAG 917
              || | | |  | ||  | | ||| ||||||  |    ||||||    | | ||  || |
Db        487 GCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCCATCACGGGCCAGGTCCCCCG 546

Qy        918 GGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGG 977
              || | |     | |   |  |||| ||||  | || | | | ||| ||  |
Db        547 CCGCATGATCGGCACCGACGCCTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTCCAT 606

Qy        978 CACAATG 984
              ||| | |
Db        607 CACCAAG 613


RESULT 7
US-10-509-121-1
; Sequence 1, Application US/10509121
; Publication No. US20050283855A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU, et al.
;  TITLE OF INVENTION: GENE CODING FOR ACETOLACTATE SYNTHASE
;  FILE REFERENCE: 1254-0259PUS1
;  CURRENT APPLICATION NUMBER: US/10/509,121
;  CURRENT FILING DATE:  2004-09-28
;  PRIOR APPLICATION NUMBER: JP 2002-95721
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 2301
;   TYPE: DNA
;   ORGANISM: Oryza sativa var. kinmaze
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (48)..(1979)
US-10-509-121-1

  Query Match             2.5%;  Score 35;  DB 7;  Length 2301;
  Best Local Similarity   49.2%;  Pred. No. 4.1;
  Matches   92;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        798 CGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGG 857
              || |  |   |  |||   || | || |||||  |  |   |||   ||  |      |
Db        443 CGGCCGCGTCGGGGTCTGCGTCGCCACCTCCGGCCCCGGGGCAACCAACCTCGTGTCCGC 502

Qy        858 AGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAG 917
              || | | |  | ||  | | ||| ||||||  |    ||||||    | | ||  |||
Db        503 GCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCCATCACGGGCCAGGTCCACAG 562

Qy        918 GGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGG 977
              || | |     | |   |  |||| ||||  | || | | | ||| ||  |
Db        563 CCGCATGATCGGCACCGACGCCTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTCCAT 622

Qy        978 CACAATG 984
              ||| | |
Db        623 CACCAAG 629


RESULT 8
US-10-509-121-38
; Sequence 38, Application US/10509121
; Publication No. US20050283855A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU, et al.
;  TITLE OF INVENTION: GENE CODING FOR ACETOLACTATE SYNTHASE
;  FILE REFERENCE: 1254-0259PUS1
;  CURRENT APPLICATION NUMBER: US/10/509,121
;  CURRENT FILING DATE:  2004-09-28
;  PRIOR APPLICATION NUMBER: JP 2002-95721
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
;   LENGTH: 2301
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;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-10-509-121-38

  Query Match             2.5%;  Score 35;  DB 7;  Length 2301;
  Best Local Similarity   49.2%;  Pred. No. 4.1;
  Matches   92;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        798 CGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGG 857
              || |  |   |  |||   || | || |||||  |  |   |||   ||  |       |
Db        443 CGGCCGCGTCGGGGTCTGCGTCGCCACCTCCGGCCCCGGGGCAACCAACCTCGTGTCCGC 502

Qy        858 AGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAG 917
                || | | |  | ||  | | ||| ||||||  |    ||||||    | | || || |
Db        503 GCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCCATCACGGGCCAGGTCCCCCG 562

Qy        918 GGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGG 977
                || | |       | |   |  |||| ||||  | || | | | ||| ||  |
Db        563 CCGCATGATCGGCACCGACGCCTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTCCAT 622

Qy        978 CACAATG 984
              |||  | |
Db        623 CACCAAG 629


RESULT 9
US-10-601-368-20
; Sequence 20, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  APPLICANT:  Lora, Jose M.
;  TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
;  FILE REFERENCE: 07334-275001
;  CURRENT APPLICATION NUMBER: US/10/601,368
;  CURRENT FILING DATE:  2003-06-23
;  PRIOR APPLICATION NUMBER: US/09/561,263A
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: US 09/322,790
;  PRIOR FILING DATE: 1999-05-28
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
;   LENGTH: 3564
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(3564)
US-10-601-368-20

  Query Match             2.4%;  Score 34;  DB 7;  Length 3564;
  Best Local Similarity   56.1%;  Pred. No. 11;
  Matches   64;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              | ||||  ||| | ||| ||    |||| ||| |  | |||   ||  ||||||     |
Db       2602 AGCCTGATCCAGAAGGATGACTCAGACAACAGCATCGAGTGTGTGAACGAGGAGAGGCGG 2661

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACG 1314
                |  | ||||| |||||  | |      |||||  ||| | |  | ||| |
Db       2662 CTTCACAAGAAAGTCTGCAACGTCAGCTACCCCTTCTTCAGAGCCAAGGCCAAG 2715


RESULT 10
US-10-601-368-19
; Sequence 19, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  APPLICANT:  Lora, Jose M.
;  TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
;  FILE REFERENCE: 07334-275001
;  CURRENT APPLICATION NUMBER: US/10/601,368
;  CURRENT FILING DATE:  2003-06-23
;  PRIOR APPLICATION NUMBER: US/09/561,263A
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: US 09/322,790
;  PRIOR FILING DATE: 1999-05-28
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 4858
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (28)...(3591)
US-10-601-368-19

  Query Match             2.4%;  Score 34;  DB 7;  Length 4858;
  Best Local Similarity   56.1%;  Pred. No. 13;
  Matches   64;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              | ||||  ||| | ||| ||    |||| ||| |  | |||   ||  ||||||     |
Db       2629 AGCCTGATCCAGAAGGATGACTCAGACAACAGCATCGAGTGTGTGAACGAGGAGAGGCGG 2688

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACG 1314
                |  | ||||| |||||  | |      |||||  ||| | |  | ||| |
Db       2689 CTTCACAAGAAAGTCTGCAACGTCAGCTACCCCTTCTTCAGAGCCAAGGCCAAG 2742


RESULT 11
US-10-509-121-5
; Sequence 5, Application US/10509121
; Publication No. US20050283855A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU, et al.
;  TITLE OF INVENTION: GENE CODING FOR ACETOLACTATE SYNTHASE
;  FILE REFERENCE: 1254-0259PUS1
;  CURRENT APPLICATION NUMBER: US/10/509,121
;  CURRENT FILING DATE:  2004-09-28
;  PRIOR APPLICATION NUMBER: JP 2002-95721
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 2294
;   TYPE: DNA
;   ORGANISM: Oryza sativa var. kinmaze
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (48)..(1979)
US-10-509-121-5

  Query Match             2.4%;  Score 33.4;  DB 7;  Length 2294;
  Best Local Similarity   48.7%;  Pred. No. 13;
  Matches   91;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        798 CGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGG 857
              || |  |   |  |||   || | || |||||  |  |   |||   ||  |       |
Db        443 CGGCCGCGTCGGGGTCTGCGTCGCCACCTCCGGCCCCGGGGCAACCAACCTCGTGTCCGC 502

Qy        858 AGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAG 917
                || | | |  | ||  | | ||| ||||||  |    ||||||    | | || || |
Db        503 GCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCCATCACGGGCCAGGTCCACCG 562

Qy        918 GGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGG 977
                || | |       | |   |  |||| ||||  | || | | | ||| ||  |
Db        563 CCGCATGATCGGCACCGACGCCTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTCCAT 622

Qy        978 CACAATG 984
              |||  | |
Db        623 CACCAAG 629
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RESULT 12
US-10-509-121-7
; Sequence 7, Application US/10509121
; Publication No. US20050283855A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU, et al.
;  TITLE OF INVENTION: GENE CODING FOR ACETOLACTATE SYNTHASE
;  FILE REFERENCE: 1254-0259PUS1
;  CURRENT APPLICATION NUMBER: US/10/509,121
;  CURRENT FILING DATE:  2004-09-28
;  PRIOR APPLICATION NUMBER: JP 2002-95721
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 2294
;   TYPE: DNA
;   ORGANISM: Oryza sativa var. kinmaze
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (48)..(1979)
US-10-509-121-7

  Query Match             2.4%;  Score 33.4;  DB 7;  Length 2294;
  Best Local Similarity   48.7%;  Pred. No. 13;
  Matches   91;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        798 CGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGG 857
              || |  |   |  |||   || | || |||||  |  |   |||   ||  |      |
Db        443 CGGCCGCGTCGGGGTCTGCGTCGCCACCTCCGGCCCCGGGGCAACCAACCTCGTGTCCGC 502

Qy        858 AGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAG 917
              || | | |  | ||  | | ||| ||||||  |    ||||||    | | ||  | |
Db        503 GCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCCATCACGGGCCAGGTCCACCG 562

Qy        918 GGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGG 977
              || | |       | |   |  |||| ||||  | || | | | ||| ||  |
Db        563 CCGCATGATCGGCACCGACGCCTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTCCAT 622

Qy        978 CACAATG 984
              |||  | |
Db        623 CACCAAG 629


RESULT 13
US-10-509-121-3
; Sequence 3, Application US/10509121
; Publication No. US20050283855A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU, et al.
;  TITLE OF INVENTION: GENE CODING FOR ACETOLACTATE SYNTHASE
;  FILE REFERENCE: 1254-0259PUS1
;  CURRENT APPLICATION NUMBER: US/10/509,121
;  CURRENT FILING DATE:  2004-09-28
;  PRIOR APPLICATION NUMBER: JP 2002-95721
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2300
;   TYPE: DNA
;   ORGANISM: Oryza sativa var. kinmaze
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (48)..(1979)
US-10-509-121-3

  Query Match             2.4%;  Score 33.4;  DB 7;  Length 2300;
  Best Local Similarity   48.7%;  Pred. No. 13;
  Matches   91;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        798 CGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGG 857
              || |  |   |  |||   || | || |||||  |  |   |||   ||  |      |
Db        443 CGGCCGCGTCGGGGTCTGCGTCGCCACCTCCGGCCCCGGGGCAACCAACCTCGTGTCCGC 502

Qy        858 AGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAG 917
              || | | |  | ||  | | ||| ||||||  |    ||||||    | | ||  | |
Db        503 GCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCCATCACGGGCCAGGTCCACCG 562

Qy        918 GGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGG 977
              || | |       | |   |  |||| ||||  | || | | | ||| ||  |
Db        563 CCGCATGATCGGCACCGACGCCTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTCCAT 622

Qy        978 CACAATG 984
              |||  | |
Db        623 CACCAAG 629


RESULT 14
US-10-649-457-1
; Sequence 1, Application US/10649457
; Publication No. US20060019380A1
; GENERAL INFORMATION:
;  APPLICANT: Crystal, Ronald G
;  APPLICANT:  Hackett, Neil R
;  APPLICANT:  Tan, Yadi
;  TITLE OF INVENTION: GENETIC VACCINES DIRECTED AGAINST BACTERIAL EXOTOXINS
;  FILE REFERENCE: 216474
;  CURRENT APPLICATION NUMBER: US/10/649,457
;  CURRENT FILING DATE:  2003-08-27
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 2295
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic B. anthracis gene for protective antigen with
;   OTHER INFORMATION: human-preferred codons
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2295)
US-10-649-457-1

  Query Match             2.3%;  Score 33;  DB 6;  Length 2295;
  Best Local Similarity   47.0%;  Pred. No. 17;
  Matches  102;  Conservative    0;  Mismatches  115;  Indels    0;  Gaps    0;

Qy       1010 CAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGA 1069
              | |||| ||      ||  |  ||||||     | | | | ||||||      ||||
Db       1193 CCGGGACCGCCCCCATCTACAACGTGCTGCCCACCACCTCCCTGGTGCTGGGCAAGAACC 1252

Qy       1070 TGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACC 1129
              ||| |    | |||||  | ||   |        |   | | |   |||  ||| |||
Db       1253 AGACCCTCGCGACCATCAAGGCCAAGGAGAACCAGCTGAGCCAGATCCTGGCCCCCAACA 1312

Qy       1130 CAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACT 1189
                |    | |   || |   || | | |   | | | ||| ||  || |   ||| ||
Db       1313 ACTACTATCCCTCCAAGAACTTGGCGCCCATCGCCCTGAACGCCCAGGACGACTTCAGCT 1372

Qy       1190 ATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGA 1226
                ||   || | | ||  | |||   |   |||||
Db       1373 CCACCCCCATCACCATGAACTACAACCAGTTCCTGGA 1409


RESULT 15
US-11-124-368A-2921/c
; Sequence 2921, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  James J. Devlin
;  APPLICANT:  May Luke
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Vascular Diseases, Methods of Detection and Uses Thereof
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; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2921
; LENGTH: 98309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-2921

Query Match 2.3%; Score 33; DB 8; Length 98309;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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Qy        856 GGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACC 915
              |||| |||  | |   | || |    |  |  | | | ||   | ||| | |||| || |
Db      11288 GGAGCCTCTCCAACCTTCACTCTCATCCCCATGGCTGGGAGGTTGACAGACCCGAGCATC 11229

Qy        916 AGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTG 975
              || |  | ||| |  || || ||  ||| |   || |   |  |  ||  | |||||||
Db      11228 AGAGAAACCCTGGCCCACCAGCTCTGCCATCTTCCACCCTGCCACCTCGCTGTCACCCTG 11169

Qy        976 G 976
              |
Db      11168 G 11168
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Job time : 331 secs

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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 14:19:20 ; Search time 287 Seconds
(without alignments)
8751.549 Million cell updates/sec

Title: US-10-733-031-5
Perfect score: 1413
Sequence: 1 aacaccaacaaggcaaccgc.....tggcagcaccactcatcgga 1413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1390.6	98.4	3097	3	US-09-282-147-38	Sequence 38, Appl
2	1390.6	98.4	3097	3	US-10-216-981A-2	Sequence 2, Appli
3	1327.4	93.9	1553	9	5165925-3	Patent No. 5165925
4	994.4	70.4	3097	3	US-09-282-147-36	Sequence 36, Appl
5	262.6	18.6	3264	2	US-08-708-541A-31	Sequence 31, Appl
6	262.6	18.6	3264	2	US-08-708-541A-33	Sequence 33, Appl
7	262.6	18.6	3264	3	US-09-147-771-31	Sequence 31, Appl
8	262.6	18.6	3264	3	US-09-147-771-33	Sequence 33, Appl
9	240.6	17.0	1471	2	US-08-216-276A-15	Sequence 15, Appl
10	239.2	16.9	3180	2	US-07-944-943-1	Sequence 1, Appli
11	239	16.9	1471	6	PCT-US91-03056-15	Sequence 15, Appl
12	238.8	16.9	3180	2	US-07-944-525-1	Sequence 1, Appli
13	238.8	16.9	3180	2	US-08-219-262B-13	Sequence 13, Appl
14	238.8	16.9	3180	3	US-09-031-655-13	Sequence 13, Appl
15	237.2	16.8	3230	2	US-08-219-262B-11	Sequence 11, Appl
16	237.2	16.8	3230	3	US-09-031-655-11	Sequence 11, Appl
17	237.2	16.8	3230	6	PCT-US91-03056-16	Sequence 16, Appl
18	235.6	16.7	3230	2	US-08-216-276A-18	Sequence 18, Appl
19	234	16.6	3261	2	US-08-708-541A-27	Sequence 27, Appl
20	234	16.6	3261	2	US-08-708-541A-29	Sequence 29, Appl
21	234	16.6	3261	3	US-08-940-968-23	Sequence 23, Appl
22	234	16.6	3261	3	US-09-147-771-27	Sequence 27, Appl
23	234	16.6	3261	3	US-09-147-771-29	Sequence 29, Appl
24	223.4	15.8	1374	3	US-09-964-895-1	Sequence 1, Appli
25	222.8	15.8	3257	9	5223424-9	Patent No. 5223424
26	220.2	15.6	1365	3	US-09-450-433-1	Sequence 1, Appli
27	216.4	15.3	3054	3	US-09-477-574A-1	Sequence 1, Appli
28	214.2	15.2	1362	3	US-09-232-479-13	Sequence 13, Appl
29	214.2	15.2	1362	3	US-09-784-990-13	Sequence 13, Appl
30	214.2	15.2	1374	3	US-09-964-895-16	Sequence 16, Appl
31	204.8	14.5	3350	2	US-08-663-566A-1	Sequence 1, Appli
32	204.8	14.5	3350	2	US-08-023-610-1	Sequence 1, Appli
33	204.8	14.5	3350	2	US-08-288-065A-1	Sequence 1, Appli
34	204.8	14.5	3350	2	US-08-362-240A-1	Sequence 1, Appli
35	204.8	14.5	3350	6	PCT-US95-10245-1	Sequence 1, Appli
36	147.4	10.4	1622	2	US-08-216-276A-30	Sequence 30, Appl
37	112.2	7.9	1078	3	US-09-888-876-1	Sequence 1, Appli
38	109	7.7	970	2	US-08-216-276A-28	Sequence 28, Appl
39	108.2	7.7	420	3	US-09-450-433-2	Sequence 2, Appli
40	101.8	7.2	440	3	US-09-450-433-3	Sequence 3, Appli
41	68.4	4.8	348	2	US-08-216-276A-26	Sequence 26, Appl
42	45.4	3.2	119	2	US-08-708-541A-8	Sequence 8, Appli
43	45.4	3.2	119	3	US-09-147-771-8	Sequence 8, Appli
44	45.4	3.2	120	2	US-08-708-541A-7	Sequence 7, Appli
45	45.4	3.2	120	3	US-09-147-771-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-282-147-38
; Sequence 38, Application US/09282147
; Patent No. 6274147
; GENERAL INFORMATION:
; APPLICANT: VAKHARIA, Vikram
; APPLICANT: YAO, Kun
; TITLE OF INVENTION: METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS
; TITLE OF INVENTION: PANCREATIC NECROSIS VIRUS (IPNV) FROM SYNTHETIC RNA
; TITLE OF INVENTION: TRANSCRIPTS
; FILE REFERENCE: 8288-9023
; CURRENT APPLICATION NUMBER: US/09/282,147
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: US/60/080,278
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: PCT/US97/12955
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Infectious pancreatic necrosis virus
US-09-282-147-38

Query Match 98.4%; Score 1390.6; DB 3; Length 3097;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        122 AACACAAACAAGGCAACCGCAACTTACTTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        182 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACAAGAGACCTCGTCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AACTTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 301

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
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Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGTTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        482 AACGCTGCCACCTTCGAGGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAGCCATACGTCCGCCTAGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGGGCC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        782 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACGACAGTGACGGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        842 ATAAACTTCAGTCTGGCAGAACAACCCGCAGTCGAGACCAAGTTCGACTTCCAGCTGGAC 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        902 TTCATGGGCCTTGACAACGACGTCCCAGTCGTCACAGTGGTCAGCTCCGTGCTGGCCACA 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1441

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1501

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
              ||||||||||||||||||||||||||||| |||
Db       1502 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1534


RESULT 2
US-10-216-981A-2
; Sequence 2, Application US/10216981A
; Patent No. 6936256
; GENERAL INFORMATION:
;  APPLICANT: VIKHARIA, VIKRAM N
;  TITLE OF INVENTION: SUB-UNIT VACCINE FOR INFECTIOUS PANCREATIC NECROSIS VIRUS
;  FILE REFERENCE: 4115-154
;  CURRENT APPLICATION NUMBER: US/10/216,981A
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: 60/311,488
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 3097
;   TYPE: DNA
;   ORGANISM: Infectious pancreatic necrosis virus
US-10-216-981A-2

  Query Match            98.4%;  Score 1390.6;  DB 3;  Length 3097;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 1399;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              ||||| |||||||||||||||||||||| |||||||||| ||||||||||||||||||||
Db        122 AACACAAACAAGGCAACCGCAACTTACCTGAAATCCATTATGCTTCCAGAGACTGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        182 GCAAGCATCCCGGACGACATAACGGAGAGACACATCTTAAAACAAGAGACCTCGTCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AACTTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 301

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
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Db        302 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AAATATGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 481

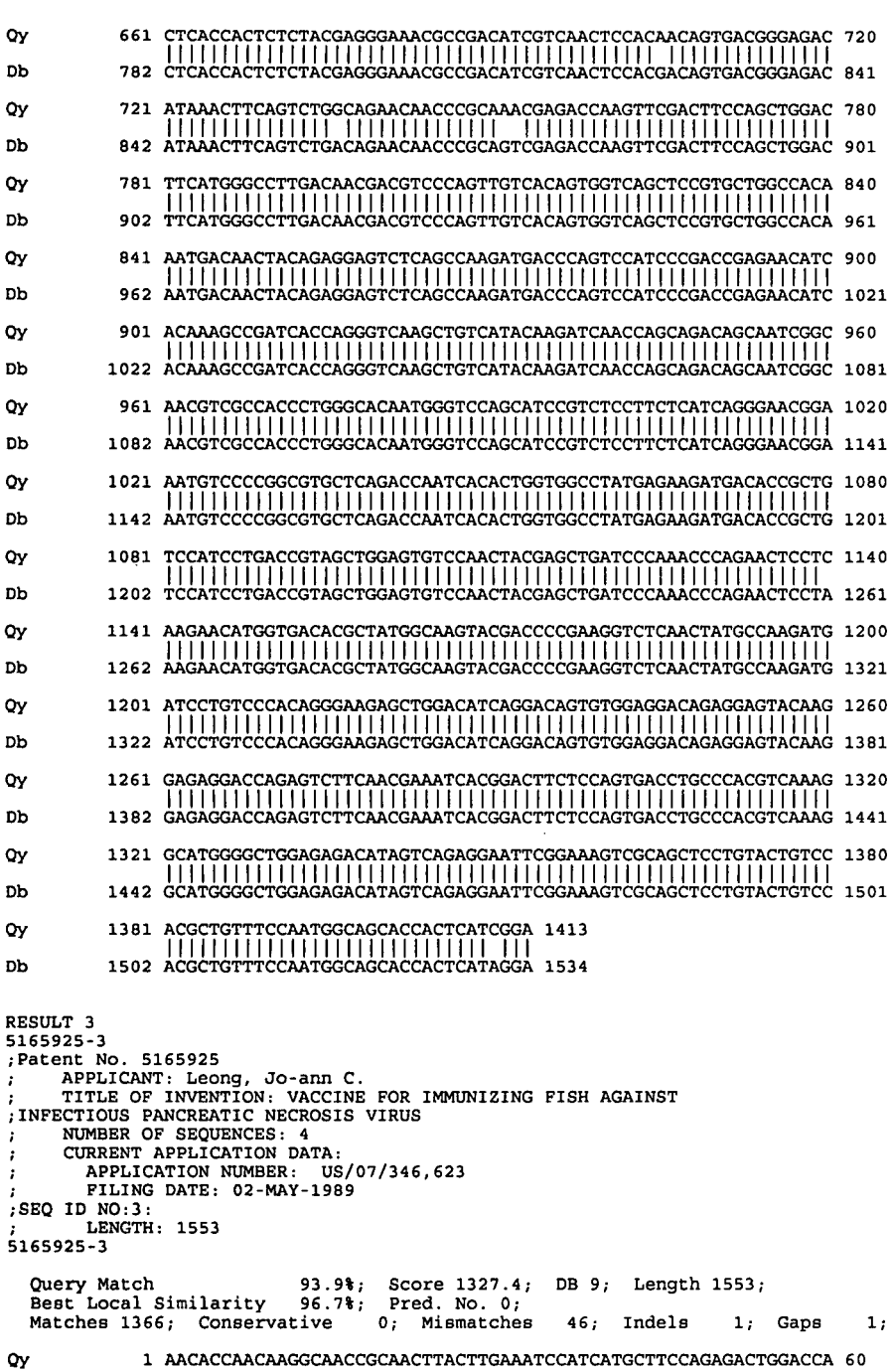
Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 661

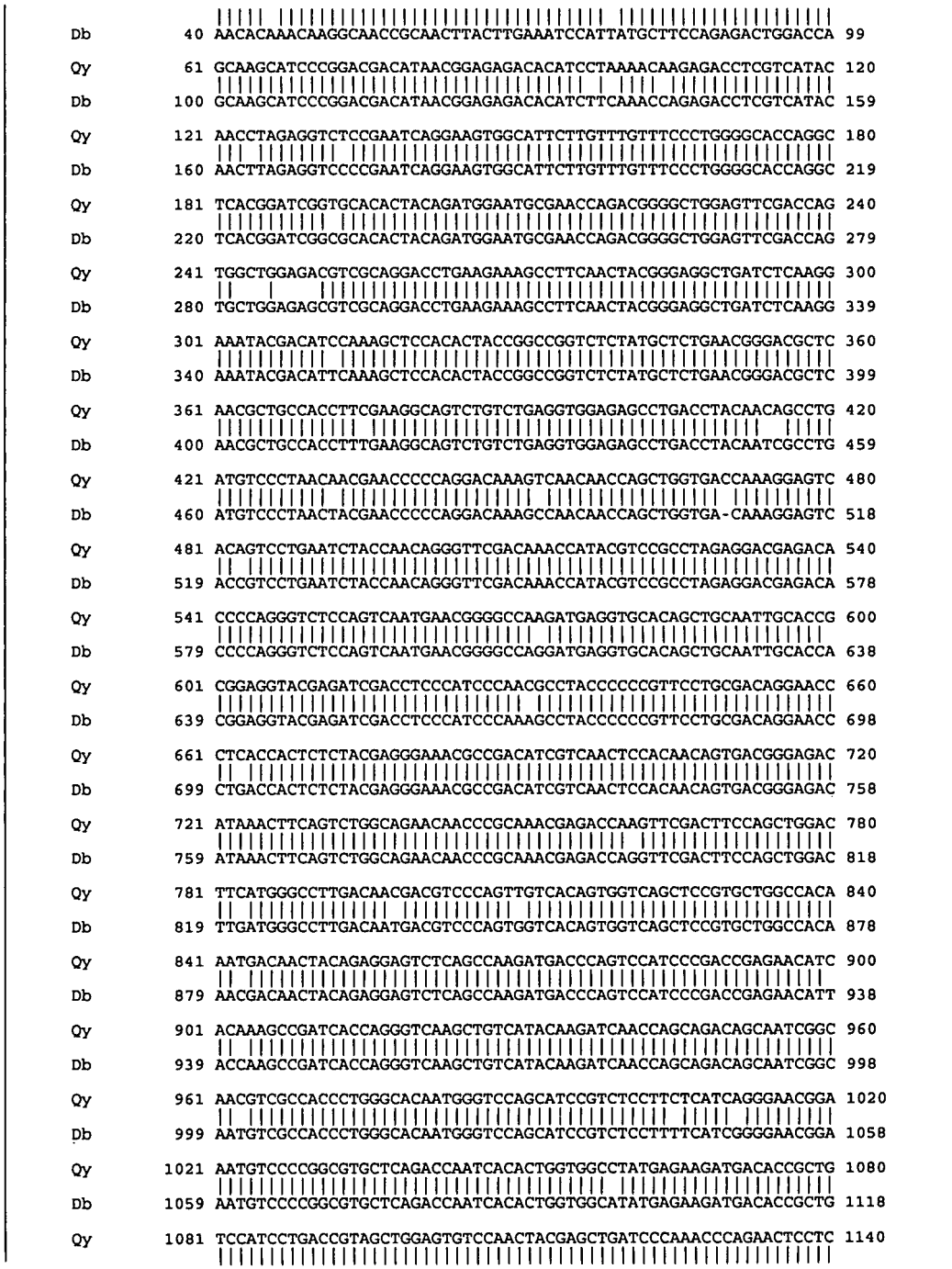
Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        662 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAACTGCACCG 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        722 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTACTGCGACAGGAACC 781
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RESULT 3
5165925-3
;Patent No. 5165925
; APPLICANT: Leong, Jo-ann C.
; TITLE OF INVENTION: VACCINE FOR IMMUNIZING FISH AGAINST
;INFECTIOUS PANCREATIC NECROSIS VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,623
; FILING DATE: 02-MAY-1989
;SEQ ID NO:3:
; LENGTH: 1553
5165925-3

Query Match 93.9%; Score 1327.4; DB 9; Length 1553;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1366; Conservative 0; Mismatches 46; Indels 1; Gaps 1;



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Db       1119 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1178

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1238

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1298

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
             |||||||||||||||||||||||||||||  ||      |||||||||||||||||||||||
Db       1299 GAGAGGACCAGAGTCTTCAACGAAATCACAGAGAAGACCAGTGACCTGCCCACGTCAAAG 1358

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
             |||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
Db       1359 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGAAAAATCGCAGCTCCTGTACTGTCC 1418

Qy       1381 ACGCTGTTTCCAATGGCAGCACCACTCATCGGA 1413
             |||||||||||||||||||||||||||||| |||
Db       1419 ACGCTGTTTCCAATGGCAGCACCACTCATAGGA 1451


RESULT 4
US-09-282-147-36
; Sequence 36, Application US/09282147
; Patent No. 6274147
; GENERAL INFORMATION:
;  APPLICANT: VAKHARIA, Vikram
;  APPLICANT: YAO, Kun
;  TITLE OF INVENTION: METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS
;  TITLE OF INVENTION: PANCREATIC NECROSIS VIRUS (IPNV) FROM SYNTHETIC RNA
;  TITLE OF INVENTION: TRANSCRIPTS
;  FILE REFERENCE: 8288-9023
;  CURRENT APPLICATION NUMBER: US/09/282,147
;  CURRENT FILING DATE: 1999-03-31
;  EARLIER APPLICATION NUMBER: US/60/080,278
;  EARLIER FILING DATE: 1998-03-31
;  EARLIER APPLICATION NUMBER: PCT/US97/12955
;  EARLIER FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 3097
;   TYPE: DNA
;   ORGANISM: Infectious pancreatic necrosis virus
US-09-282-147-36

  Query Match            70.4%;  Score 994.4;  DB 3;  Length 3097;
  Best Local Similarity  81.5%;  Pred. No. 2.7e-264;
  Matches 1151;  Conservative    0;  Mismatches  261;  Indels    0;  Gaps    0;

Qy          1 AACACCAACAAGGCAACCGCAACTTACTTGAAATCCATCATGCTTCCAGAGACTGGACCA 60
              |||||  |  ||||||||||||||||||||| |||||| |||||||| |||| |||||||
Db        122 AACACAACAAAGGCAACCGCAACTTACTTGAGATCCATTATGCTTCCCGAGAATGGACCA 181

Qy         61 GCAAGCATCCCGGACGACATAACGGAGAGACACATCCTAAAACAAGAGACCTCGTCATAC 120
              |||||||| |||||||||||||| |||||||||| |||||||||||||||| ||||||
Db        182 GCAAGCATTCCGGACGACATAACAGAGAGACACATACTAAAACAAGAGACCTCATCATAC 241

Qy        121 AACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCTTGTTTGTTTCCCTGGGGCACCAGGC 180
              ||| |||||||||||| |||||||||| |||||||| || ||||||||||| || ||
Db        242 AACTTAGAGGTCTCCGACTCAGGAAGTGGGCTTCTTGTCTGCTTCCCTGGGGCTCCCGGA 301

Qy        181 TCACGGATCGGTGCACACTACAGATGGAATGCGAACCAGACGGGGCTGGAGTTCGACCAG 240
              ||  |  |||||||| |||||||| |||||| ||||||||||  ||||| |||||||||
Db        302 TCCAGAGTCGGTGCCCACTACAGGTGGAATCTGAACCAGACGGAACTGGAATTCGACCAG 361

Qy        241 TGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTTCAACTACGGGAGGCTGATCTCAAGG 300
              ||| |||| || || |||||||||||||||| |||||||||||||| |||||||| ||
Db        362 TGGTTGGAAACATCACAGGACCTGAAGAAAGCATTCAACTACGGGAGGTTGATCTCACGG 421

Qy        301 AAATACGACATCCAAAGCTCCACACTACCGGCCGGTCTCTATGCTCTGAACGGGACGCTC 360
              |||||||||||||| ||||| || || || || || |||||||| || |||||||| ||
Db        422 AAATACGACATCCAGAGCTCGACCCTTCCCGCTGGCCTCTATGCACTCAACGGGACCCTG 481

Qy        361 AACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGTGGAGAGCCTGACCTACAACAGCCTG 420
              || || || |||||||||| ||||| |||||||||||||||||||||| |||||| ||
Db        482 AATGCAGCTACCTTCGAAGGAAGTCTTTCTGAGGTGGAGAGCCTGACCTATAACAGCTTG 541

Qy        421 ATGTCCCTAACAACGAACCCCCAGGACAAAGTCAACAACCAGCTGGTGACCAAAGGAGTC 480
              |||||||| ||||| ||||| |||||||| |||||||||| || |||||||||||| |
Db        542 ATGTCCCTGACAACAAACCCTCAGGACAAGGTCAACAACCAACTAGTGACCAAAGGAATA 601

Qy        481 ACAGTCCTGAATCTACCAACAGGGTTCGACAAACCATACGTCCGCCTAGAGGACGAGACA 540
              || |||||||| || ||||| ||||| ||||| |||||||||||||| ||||||||||||
Db        602 ACCGTCCTGAACCTTCCAACTGGGTTTGACAAGCCATACGTCCGCCTTGAGGACGAGACA 661

Qy        541 CCCCAGGGTCTCCAGTCAATGAACGGGGCCAAGATGAGGTGCACAGCTGCAATTGCACCG 600
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Db        662 CCGCAGGGCCCCCAGTCCATGAACGGAGCCAGGATGAGGTGCACCGCTGCAATCGCACCA 721

Qy        601 CGGAGGTACGAGATCGACCTCCCATCCCAACGCCTACCCCCCGTTCCTGCGACAGGAACC 660
              |||||||||| || |||||||||||  | ||||||||  ||||  | || || || |||
Db        722 AGGAGGTACGAAATAGACCTCCCATCTGAGCGCCTACCAACCGTGGCAGCAACTGGGACC 781

Qy        661 CTCACCACTCTCTACGAGGGAAACGCCGACATCGTCAACTCCACAACAGTGACGGGAGAC 720
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Db        782 CCAACAACAATCTATGAAGGGAACGCCGACATTGTGAACTCAACCACAGTGACAGGAGAC 841

Qy        721 ATAAACTTCAGTCTGGCAGAACAACCCGCAAACGAGACCAAGTTCGACTTCCAGCTGGAC 780
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Db        842 GTAACCTTCCAACTAGCAGCCGAACCCGTCAACGAGACGCGGTTCGACTTCATCCTACAA 901

Qy        781 TTCATGGGCCTTGACAACGACGTCCCAGTTGTCACAGTGGTCAGCTCCGTGCTGGCCACA 840
              ||| | || |||||||| || || || || ||| | |||    |||||     |||| |||
Db        902 TTCCTTGGGCTTGACAATGATGTGCCCGTGGTCTCCGTGACAAGCTCAACCCTGGTCACG 961

Qy        841 AATGACAACTACAGAGGAGTCTCAGCCAAGATGACCCAGTCCATCCCGACCGAGAACATC 900
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Db        962 GCCGACAACTACAGGGGTGCCTCCGCCAAGTTTACGCAGTCAATCCCAACGGAACTAATA 1021

Qy        901 ACAAAGCCGATCACCAGGGTCAAGCTGTCATACAAGATCAACCAGCAGACAGCAATCGGC 960
              || ||||| || || |||||||||||| | ||| || |||||||||||||| ||||||||
Db       1022 ACTAAGCCCATTACAAGGGTCAAGCTGGCTTACCAGCTCAACCAGCAGACCGCAATCGGA 1081

Qy        961 AACGTCGCCACCCTGGGCACAATGGGTCCAGCATCCGTCTCCTTCTCATCAGGGAACGGA 1020
              |||| ||| || || ||  | |  || ||  | || ||||| ||||||||||||| ||
Db       1082 AACGCCGCAACACTCGGGGCCAAAGGACCCCCGTCAGTCTCATTCTCATCAGGGAATGGC 1141

Qy       1021 AATGTCCCCGGCGTGCTCAGACCAATCACACTGGTGGCCTATGAGAAGATGACACCGCTG 1080
              ||||| || || || || ||||| || ||  ||||||| || || |||||||| || | |
Db       1142 AATGTGCCGGGGGTTCTAAGACCCATAACCTTGGTGGCATACGAAAAGATGACCCCCCAG 1201

Qy       1081 TCCATCCTGACCGTAGCTGGAGTGTCCAACTACGAGCTGATCCCAAACCCAGAACTCCTC 1140
              || || |||||||| || || || |||||||| |||||||||| |||||||| |||||
Db       1202 TCAATTCTGACCGTGGCCGGCGTATCCAACTATGAGCTGATCCCCAACCCAGACCTCCTG 1261

Qy       1141 AAGAACATGGTGACACGCTATGGCAAGTACGACCCCGAAGGTCTCAACTATGCCAAGATG 1200
              |||||||||| ||     |||||||| || ||||| || || ||||||||||||||||||
Db       1262 AAGAACATGGTCACCAAGTATGGCAAATATGACCCTGAGGGCCTCAACTATGCCAAGATG 1321

Qy       1201 ATCCTGTCCCACAGGGAAGAGCTGGACATCAGGACAGTGTGGAGGACAGAGGAGTACAAG 1260
              |||||||||||||||| ||||| ||||| || || || |||||||| ||||||||||||
Db       1322 ATCCTGTCCCACAGGGAGGAGCTAGACATTAGAACTGTCTGGAGGACCGAGGAGTACAAG 1381

Qy       1261 GAGAGGACCAGAGTCTTCAACGAAATCACGGACTTCTCCAGTGACCTGCCCACGTCAAAG 1320
              |||||||| |||| |||||| || ||||| |||||| | |||||||||| || |||||
Db       1382 GAGAGGACAAGAGCCTTCAATGAGATCACTGACTTCACAAGTGACCTGCCAACATCAAAA 1441

Qy       1321 GCATGGGGCTGGAGAGACATAGTCAGAGGAATTCGGAAAGTCGCAGCTCCTGTACTGTCC 1380
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Db       1502 ACGCTCTTCCCAATGGCCGCCCCACTTATAGG 1533


RESULT 5
US-08-708-541A-31
; Sequence 31, Application US/08708541A
; Patent No. 5871744
;  GENERAL INFORMATION:
;    APPLICANT:  VAKHARIA, Vikram N.
;    APPLICANT:  MUNDT, Egbert
;    TITLE OF INVENTION:  A METHOD FOR GENERATING BIRNAVIRUS FROM
;    TITLE OF INVENTION:  SYNTHETIC RNA TRANSCRIPTS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
;      STREET:  655 Fifteenth Street, N. W.,
;      STREET:  Suite 330 - G Street Lobby
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/708,541A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITTS, Monica C.
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P8172-6002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/638-5000
;      TELEFAX:  202/638-4810
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3264 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  97..531
US-08-708-541A-31

  Query Match             18.6%;  Score 262.6;  DB 2;  Length 3264;
  Best Local Similarity   52.6%;  Pred. No. 3.4e-62;
  Matches  724;  Conservative    0;  Mismatches  629;  Indels   24;  Gaps    6;

Qy          36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
               | |  || | |||  ||| ||||| ||   ||| ||||||||||     |||||  ||||
Db         181 CCTTCTGATGCCAACGACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 240

Qy          96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
               || |      || |||||| | |||||| |     ||     ||  ||||     ||  |  |
Db         241 ACTCAGGTCCGAAACCTCGACTTACAACTTGACTGTAGGGGATACAGGGTCAGGACTAAT 300

Qy         156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
               ||| | |||||||||    || || |||    | ||||| ||||||| |  | |   ||
Db         301 TGTCTTTTTCCCTGGATTCCCTGGTTCAGTTGTAGGTGCTCACTACACACTGCA---GAG 357

Qy         216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
               |      |  | |||||||||  |||   |||  ||||| |||||          ||
Db         358 CAGTGGGAACTACCAATTCGACCAGATGCTCCTGACAGCGCAGAACCTGCCTGCCAGCTA 417

Qy         276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
               |||||||  | |||||  |    ||||       | | |       ||||||  || |  ||
Db         418 CAACTACTGCAGGCTAGTGAGCAGGAGTCTAACCGTACGGTCAAGCACACTCCCTGGTGG 477

Qy         336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
               | ||||| || ||||| ||  | ||||| |  |||||| | || || |||  |||| |
Db         478 CGTTTATGCACTAAACGGAACCATAAACGCAGTGACCTTCCACGGAAGCCTGAGTGAGTT 537

Qy         396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
               |      |   | |||||||  | ||||||||     ||  |||||  | |  |||||  ||
Db         538 GACTGACTACAGCTACAACGGGCTGATGTCAGCCACTGCGAACATCAACGACAAGATCGG 597

Qy         456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
               |||   || ||    |||| || || || || | |||||| ||     |  |||
Db         598 GAACGTTCTAGTTGGAGAAGGGGTGACTGTTCTCAGTCTACCGACTTCATATGACCTTAG 657

Qy         516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
               || ||  | || |  |||   |  |||       || ||| |  | | |      |||||
Db         658 TTATGTGAGACTCGGTGACCCCATCCCCGCAGCAGGACTCGACCCGAAGTTGATGGCCAC 717

Qy         573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
               |      | |  |      |       |          |                || ||||
Db         718 GTGCGACAGTAGTGACAGACCCAGAGTCTACACCATAACAGCTGCAGATGAATACCAATT 777

Qy         633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
               |    | |   |    |||  ||      ||||| || | |   |  |||  |||
Db         778 CTCGTCACAACTCATCCCGAGTGGCGTGAAGACCACACTGTTCTCCGCCAACATCGATGC 837

Qy         693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
               |||  |   |  ||    || ||  |   ||||||  |       ||  | |      |
Db         838 TCTCACCAGCTTCAGCGTTGGTGGTGAGCTTGTCTTCAGCC------AAGTAACGATCCA 891

Qy         753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGAC---AACGACGTCCCAGT 809
                  |  | |||  ||     |  |||||| ||  ||||    |  ||||  ||||
Db         892 AAGCATTGAAGTGGACGTCACCATTCACTTCATTGGGTTTGACGGGACAGACGTAGCAGT 951

Qy         810 TGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAA 869
               |||| |  |    | |   |  |||| ||  |   |||     ||  ||  |||
Db         952 CAAGGCAGTTGCAACAGACTTTGGGCTGACAACTGGGACAAACAACCTTGTGCCATTCAA 1011

Qy         870 GATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTC 929
                 || |   |||| ||  |  | |||||  |||| |||||      | || ||
Db        1012 ------CCTGGTGGTCCCAACAAATGAGATCACCCAGCCCATCACTTCCATGAAACTAGA 1065

Qy         930 ATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCC 989
                  || | ||  ||     |  | ||     | | |  |     | ||| ||  ||
Db        1066 GGTTGTGACCTACAAGATTGGCGGCACCGCTGGTGACCCAATATCATGGACAGTGAGTGG 1125

Qy         990 AGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCAC 1049
                 ||   |  |  |  |           || ||   ||| || |  ||| | ||  ||||
Db        1126 TACAC---TAGCTGTGACGGTGCACGGAGGCAACTACCCTGGGGCTCTCCGTCCTGTCAC 1182

Qy        1050 ACTGGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAA 1109
               |||||||||||||||     ||  |  |    ||  |  | || || || || ||| |||
Db        1183 CCTGGTGGCCTATGAACGAGTGGCTGCAGGATCTGTTGTCACAGTTGCAGGGGTGAGCAA 1242

Qy        1110 CTACGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTA 1169
               || |||||| ||||| ||||| || ||    ||||||  | || |||   ||||||   |
Db        1243 CTTCGAGCTAATCCCCAACCCTGAGCTTGCAAAGAACCTAGTTACAGAGTATGGCCGCTT 1302

Qy        1170 CGACCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACAT 1229
               |||||||  ||   | |||||  ||||  | || |||    | || ||    || | |||
Db        1303 TGACCCCGGAGCAATGAACTACACCAAACTAATACTGAGTGAGAGAGATCGTCTAGGCAT 1362

Qy        1230 CAGGACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCAC 1289
               || |||||| |||    ||   ||||||||  ||      |||||  ||  |  |
Db        1363 CAAGACAGTCTGGCCCACCAGGGAGTACACCGATTTCAGGGAGTACTTCATGGAGGTTGC 1422

Qy        1290 GGACTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGG 1349
               ||  ||  |    |||   |  ||   ||||  ||||  |  |||||| || |||
Db        1423 AGATCTCAACTCACCCCTAAAGATTGCAGGAGCATTTGGCTTTAAGGACATAATCCGAGC 1482

Qy        1350 AATTCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
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RESULT 6
US-08-708-541A-33
; Sequence 33, Application US/08708541A
; Patent No. 5871744
;  GENERAL INFORMATION:
;    APPLICANT:  VAKHARIA, Vikram N.
;    APPLICANT:  MUNDT, Egbert
;    TITLE OF INVENTION:  A METHOD FOR GENERATING BIRNAVIRUS FROM
;    TITLE OF INVENTION:  SYNTHETIC RNA TRANSCRIPTS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
;      STREET:  655 Fifteenth Street, N. W.,
;      STREET:  Suite 330 - G Street Lobby
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/708,541A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITTS, Monica C.
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P8172-6002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/638-5000
;      TELEFAX:  202/638-4810
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3264 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  131..3169
US-08-708-541A-33

  Query Match             18.6%;  Score 262.6;  DB 2;  Length 3264;
  Best Local Similarity   52.6%;  Pred. No. 3.4e-62;
  Matches  724;  Conservative    0;  Mismatches  629;  Indels   24;  Gaps    6;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
Db        181 CCTTCTGATGCCAACGACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 240

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
Db        241 ACTCAGGTCCGAAACCTCGACTTACAACTTGACTGTAGGGGATACAGGGTCAGGACTAAT 300

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
Db        301 TGTCTTTTTCCCTGGATTCCCTGGTTCAGTTGTAGGTGCTCACTACACACTGCA---GAG 357

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
Db        358 CAGTGGGAACTACCAATTCGACCAGATGCTCCTGACAGCGCAGAACCTGCCTGCCAGCTA 417

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
Db        418 CAACTACTGCAGGCTAGTGAGCAGGAGTCTAACCGTACGGTCAAGCACACTCCCTGGTGG 477

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
pb        478 CGTTTATGCACTAAACGGAACCATAAACGCAGTGACCTTCCACGGAAGCCTGAGTGAGTT 537

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
Db        538 GACTGACTACAGCTACAACGGGCTGATGTCAGCCACTGCGAACATCAACGACAAGATCGG 597

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
Db        598 GAACGTTCTAGTTGGAGAAGGGGTGACTGTTCTCAGTCTACCGACTTCATATGACCTTAG 657

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
Db        658 TTATGTGAGACTCGGTGACCCCATCCCCGCAGCAGGACTCGACCCGAAGTTGATGGCCAC 717

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
Db        718 GTGCGACAGTAGTGACAGACCCAGAGTCTACACCATAACAGCTGCAGATGAATACCAATT 777

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
Db        778 CTCGTCACAACTCATCCCGAGTGGCGTGAAGACCACACTGTTCTCCGCCAACATCGATGC 837

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
Db        838 TCTCACCAGCTTCAGCGTTGGTGGTGAGCTTGTCTTCAGCC------AAGTAACGATCCA 891

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGAC---AACGACGTCCCAGT 809
Db        892 AAGCATTGAAGTGGACGTCACCATTCACTTCATTGGGTTTGACGGGACAGACGTAGCAGT 951

Qy        810 TGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAA 869
Db        952 CAAGGCAGTTGCAACAGACTTTGGGCTGACAACTGGGACAAACAACCTTGTGCCATTCAA 1011

Qy        870 GATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTC 929
Db       1012 ------CCTGGTGGTCCCAACAAATGAGATCACCCAGCCCATCACTTCCATGAAACTAGA 1065

Qy        930 ATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCC 989
Db       1066 GGTTGTGACCTACAAGATTGGCGGCACCGCTGGTGACCCAATATCATGGACAGTGAGTGG 1125

Qy        990 AGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCAC 1049
Db       1126 TACAC---TAGCTGTGACGGTGCACGGAGGCAACTACCCTGGGGCTCTCCGTCCTGTCAC 1182

Qy       1050 ACTGGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAA 1109
Db       1183 CCTGGTGGCCTATGAACGAGTGGCTGCAGGATCTGTTGTCACAGTTGCAGGGGTGAGCAA 1242

Qy       1110 CTACGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTA 1169
Db       1243 CTTCGAGCTAATCCCCAACCCTGAGCTTGCAAAGAACCTAGTTACAGAGTATGGCCGCTT 1302

Qy       1170 CGACCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACAT 1229
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Qy       1230 CAGGACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCAC 1289
Db       1363 CAAGACAGTCTGGCCCACCAGGGAGTACACCGATTTCAGGGAGTACTTCATGGAGGTTGC 1422

Qy       1290 GGACTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGG 1349
Db       1423 AGATCTCAACTCACCCCTAAAGATTGCAGGAGCATTTGGCTTTAAGGACATAATCCGAGC 1482

Qy       1350 AATTCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
Db       1483 CATTCGGAAGATTGCGGTGCCAGTGGTATCCACACTCTTCCCTCCAGCTGCACCCCT 1539

RESULT 7
US-09-147-771-31
; Sequence 31, Application US/09147771
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; Patent No. 6596280
;  GENERAL INFORMATION:
;    APPLICANT:  VAKHARIA, Vikram N.
;    APPLICANT:  MUNDT, Egbert
;    TITLE OF INVENTION:  A METHOD FOR GENERATING BIRNAVIRUS
;    TITLE OF INVENTION:  FROM SYNTHETIC RNA TRANSCRIPTS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARENT FOX KINTNER PLOTKIN & KAHN
;      STREET:  1050 Connecticut Ave., N.W. Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20036-5339
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/147,771
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/198,913
;      FILING DATE:  24-NOV-98
;      APPLICATION NUMBER:  PCT/US97/12955
;      FILING DATE:  31-JUL-97
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/708,541
;      FILING DATE:  05-SEP-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITTS, Monica C.
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P108288-09002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/857-6000
;      TELEFAX:  202/638-4810
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3264 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  97..531
US-09-147-771-31

  Query Match             18.6%;  Score 262.6;  DB 3;  Length 3264;
  Best Local Similarity   52.6%;  Pred. No. 3.4e-62;
  Matches  724;  Conservative    0;  Mismatches  629;  Indels   24;  Gaps    6;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
              | |  || | |||  ||| ||||| ||   ||| ||||||||||     |||||  ||||
Db        181 CCTTCTGATGCCAACGACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 240

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
               || |      || ||||||| | ||||||| |     ||     ||  ||||     ||  |  |
Db        241 ACTCAGGTCCGAAACCTCGACTTACAACTTGACTGTAGGGGATACAGGGTCAGGACTAAT 300

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
              |||  | ||||||||||     || || |||     | ||||| |||||||  |  | |   ||
Db        301 TGTCTTTTTCCCTGGATTCCCTGGTTCAGTTGTAGGTGCTCACTACACACTGCA---GAG 357

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
              |      |  | |||||||||  |||   |||  ||||| |||||           ||
Db        358 CAGTGGGAACTACCAATTCGACCAGATGCTCCTGACAGCGCAGAACCTGCCTGCCAGCTA 417

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
              |||||||  | |||||   |     ||||        | | |        ||||||  || |  ||
Db        418 CAACTACTGCAGGCTAGTGAGCAGGAGTCTAACCGTACGGTCAAGCACACTCCCTGGTGG 477

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
              | |||||  || |||||  ||   | |||||  |   ||||||  |  ||  ||  |||   |||| |
Db        478 CGTTTATGCACTAAACGGAACCATAAACGCAGTGACCTTCCACGGAAGCCTGAGTGAGTT 537

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
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Db        538 GACTGACTACAGCTACAACGGGCTGATGTCAGCCACTGCGAACATCAACGACAAGATCGG 597

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
              |||   || ||      |||| || || || || | |||||| ||     |  |||
Db        598 GAACGTTCTAGTTGGAGAAGGGGTGACTGTTCTCAGTCTACCGACTTCATATGACCTTAG 657

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
              || ||  | || |  |||    |  |||      || ||| |  | | |     |||||
Db        658 TTATGTGAGACTCGGTGACCCCATCCCCGCAGCAGGACTCGACCCGAAGTTGATGGCCAC 717

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
              |      | |  |     |     |       |                |        || ||||
Db        718 GTGCGACAGTAGTGACAGACCCAGAGTCTACACCATAACAGCTGCAGATGAATACCAATT 777

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              |    | |   |     |||  ||        ||||| || | |   |  |||  |||
Db        778 CTCGTCACAACTCATCCCGAGTGGCGTGAAGACCACACTGTTCTCCGCCAACATCGATGC 837

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
              |||  |   |  ||   || ||  |  ||||||  |     ||  | |     |
Db        838 TCTCACCAGCTTCAGCGTTGGTGGTGAGCTTGTCTTCAGCC------AAGTAACGATCCA 891

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGAC---AACGACGTCCCAGT 809
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Qy        810 TGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAA 869
              |||| |  |     | |   |  |||| ||  |  |||     ||  ||  |||
Db        952 CAAGGCAGTTGCAACAGACTTTGGGCTGACAACTGGGACAAACAACCTTGTGCCATTCAA 1011

Qy        870 GATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTC 929
                || |   |||| ||  |  | |||||  |||| |||||      | || ||
Db       1012 ------CCTGGTGGTCCCAACAAATGAGATCACCCAGCCCATCACTTCCATGAAACTAGA 1065

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              || | ||  ||      |  | ||     | | |  |     | ||| || ||
Db       1066 GGTTGTGACCTACAAGATTGGCGGCACCGCTGGTGACCCAATATCATGGACAGTGAGTGG 1125

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Qy       1050 ACTGGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAA 1109
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Db       1243 CTTCGAGCTAATCCCCAACCCTGAGCTTGCAAAGAACCTAGTTACAGAGTATGGCCGCTT 1302

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              |||||| ||   | |||||  ||||  | || |||    | || ||    || | |||
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Qy       1230 CAGGACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCAC 1289
              || |||||| |||   ||   |||||||| ||     |      |||||  ||  | |
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Qy       1290 GGACTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGG 1349
              || ||  |     |||     ||  ||||  ||||  |  |||||| || |||
Db       1423 AGATCTCAACTCACCCCTAAAGATTGCAGGAGCATTTGGCTTTAAGGACATAATCCGAGC 1482

Qy       1350 AATTCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
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Db       1483 CATTCGGAAGATTGCGGTGCCAGTGGTATCCACACTCTTCCCTCCAGCTGCACCCCT 1539
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RESULT 8
US-09-147-771-33
; Sequence 33, Application US/09147771
; Patent No. 6596280
;  GENERAL INFORMATION:
;    APPLICANT:  VAKHARIA, Vikram N.
;    APPLICANT:  MUNDT, Egbert
;    TITLE OF INVENTION:  A METHOD FOR GENERATING BIRNAVIRUS
;    TITLE OF INVENTION:  FROM SYNTHETIC RNA TRANSCRIPTS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARENT FOX KINTNER PLOTKIN & KAHN
;      STREET:  1050 Connecticut Ave., N.W. Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20036-5339
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/147,771
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/198,913
;      FILING DATE:  24-NOV-98
;      APPLICATION NUMBER:  PCT/US97/12955
;      FILING DATE:  31-JUL-97
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/708,541
;      FILING DATE:  05-SEP-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITTS, Monica C.
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P108288-09002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/857-6000
;      TELEFAX:  202/638-4810
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3264 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  131..3169
US-09-147-771-33

  Query Match             18.6%;  Score 262.6;  DB 3;  Length 3264;
  Best Local Similarity   52.6%;  Pred. No. 3.4e-62;
  Matches  724;  Conservative    0;  Mismatches  629;  Indels   24;  Gaps    6;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
              |  |  || | |||  ||| ||||| ||   ||| ||||||||||     |||||  ||||
Db        181 CCTTCTGATGCCAACGACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 240

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
                || |      || |||||| | |||||| |    ||    ||  ||||    ||  |  |
Db        241 ACTCAGGTCCGAAACCTCGACTTACAACTTGACTGTAGGGGATACAGGGTCAGGACTAAT 300

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
              ||| | |||||||||     || || |||     | ||||| |||||||  |   ||    ||
Db        301 TGTCTTTTTCCCTGGATTCCCTGGTTCAGTTGTAGGTGCTCACTACACACTGCA---GAG 357

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
              |      |      | |||||||||  |||    |||  ||||| |||||          ||
Db        358 CAGTGGGAACTACCAATTCGACCAGATGCTCCTGACAGCGCAGAACCTGCCTGCCAGCTA 417

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
              |||||| | |||||  |    ||||        | | |      ||||| || |  ||
Db        418 CAACTACTGCAGGCTAGTGAGCAGGAGTCTAACCGTACGGTCAAGCACACTCCCTGGTGG 477

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
              | ||||| || ||||| ||  | ||||| |  |||||| | || || |||  |||| |
Db        478 CGTTTATGCACTAAACGGAACCATAAACGCAGTGACCTTCCACGGAAGCCTGAGTGAGTT 537

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
              |      |  | ||||||| | ||||||||     ||  |||||  | | |||||  ||
Db        538 GACTGACTACAGCTACAACGGGCTGATGTCAGCCACTGCGAACATCAACGACAAGATCGG 597

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
              |||   || ||      |||| || || || || | ||||||  ||    |  |||
Db        598 GAACGTTCTAGTTGGAGAAGGGGTGACTGTTCTCAGTCTACCGACTTCATATGACCTTAG 657

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
              || ||  | || |  |||  |  |||      || ||| |  | | |     |||||
Db        658 TTATGTGAGACTCGGTGACCCCATCCCCGCAGCAGGACTCGACCCGAAGTTGATGGCCAC 717

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
              |       || |  |     |     |       |                 || ||||
Db        718 GTGCGACAGTAGTGACAGACCCAGAGTCTACACCATAACAGCTGCAGATGAATACCAATT 777

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              |   | |  |     |||  ||       ||||| || | |  |  |||  |||
Db        778 CTCGTCACAACTCATCCCGAGTGGCGTGAAGACCACACTGTTCTCCGCCAACATCGATGC 837

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
              |||  |  |  |  ||   || ||  | ||||||  |      ||  | |  |
Db        838 TCTCACCAGCTTCAGCGTTGGTGGTGAGCTTGTCTTCAGCC------AAGTAACGATCCA 891

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGAC---AACGACGTCCCAGT 809
              |   |  | ||| ||   |  ||||||| ||  |||||   |  |||||  ||||
Db        892 AAGCATTGAAGTGGACGTCACCATTCACTTCATTGGGTTTGACGGGACAGACGTAGCAGT 951

Qy        810 TGTCACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAA 869
              |||| |  |    | |   |  |||| ||  |   |||     ||  ||  |||
Db        952 CAAGGCAGTTGCAACAGACTTTGGGCTGACAACTGGGACAAACAACCTTGTGCCATTCAA 1011

Qy        870 GATGACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTC 929
                || |  |||| ||  |  | |||||  |||| ||||     | || ||
Db       1012 ------CCTGGTGGTCCCAACAAATGAGATCACCCAGCCCATCACTTCCATGAAACTAGA 1065

Qy        930 ATACAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCC 989
                || | || ||      | | ||      | | | |     | ||| || ||
Db       1066 GGTTGTGACCTACAAGATTGGCGGCACCGCTGGTGACCCAATATCATGGACAGTGAGTGG 1125

Qy        990 AGCATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCAC 1049
                ||    |  |  |  |          || ||   ||| || |  ||| | ||  ||||
Db       1126 TACAC---TAGCTGTGACGGTGCACGGAGGCAACTACCCTGGGGCTCTCCGTCCTGTCAC 1182

Qy       1050 ACTGGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAA 1109
              ||||||||||||||      || |  |     ||  |  | || || || || |||  |||
Db       1183 CCTGGTGGCCTATGAACGAGTGGCTGCAGGATCTGTTGTCACAGTTGCAGGGGTGAGCAA 1242

Qy       1110 CTACGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTA 1169
              || |||||| ||||| |||||  || ||      ||||||  | || |||  ||||||   |
Db       1243 CTTCGAGCTAATCCCCAACCCTGAGCTTGCAAAGAACCTAGTTACAGAGTATGGCCGCTT 1302

Qy       1170 CGACCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACAT 1229
              |||||||  ||   | |||||  ||||  | ||  |||     | ||  ||    ||  | |||
Db       1303 TGACCCCGGAGCAATGAACTACACCAAACTAATACTGAGTGAGAGAGATCGTCTAGGCAT 1362

Qy       1230 CAGGACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCAC 1289
              || |||||| |||   ||   |||||||  ||   |     |||||  ||  |  |
Db       1363 CAAGACAGTCTGGCCCACCAGGGAGTACACCGATTTCAGGGAGTACTTCATGGAGGTTGC 1422

Qy       1290 GGACTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGG 1349
              ||  ||  |     |||    |  ||  ||||  ||||  |  |||||| || |||
Db       1423 AGATCTCAACTCACCCCTAAAGATTGCAGGAGCATTTGGCTTTAAGGACATAATCCGAGC 1482
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Qy       1350 AATTCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
             ||||||||  | || |  || ||  | ||||| || || ||    || |||||  ||
Db       1483 CATTCGGAAGATTGCGGTGCCAGTGGTATCCACACTCTTCCCTCCAGCTGCACCCCT 1539


RESULT 9
US-08-216-276A-15
; Sequence 15, Application US/08216276A
; Patent No. 5595912
;  GENERAL INFORMATION:
;    APPLICANT:  VAKHARIA, VIKRAM
;    APPLICANT:  SNYDER, DAVID
;    TITLE OF INVENTION:  SPECIFIC DNA AND RNA SEQUENCES
;    TITLE OF INVENTION:  ASSOCIATED WITH US IBDV VARIANTS, VECTOR CARRYING DNA
;    TITLE OF INVENTION:  SEQUENCES, HOST CARRYING CLONED VECTOR, DEDUCED AMINO ACID
;    TITLE OF INVENTION:  SEQUENCES, VACCINE AND METHOD OF VACCINATION
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/216,276A
;      FILING DATE:  23-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/083,784
;      FILING DATE:  28-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/519,202
;      FILING DATE:  04-MAY-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/227,311
;      FILING DATE:  02-AUG-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kelber, Steven B.
;      REGISTRATION NUMBER:  30,073
;      REFERENCE/DOCKET NUMBER:  2747-054-27 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1471 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Infectious bursal disease virus
;      STRAIN:  Delaware
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..15
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..1470
US-08-216-276A-15

  Query Match             17.0%;  Score 240.6;  DB 2;  Length 1471;
  Best Local Similarity   51.1%;  Pred. No. 3e-56;
  Matches  701;  Conservative    0;  Mismatches  649;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
              |  || | |||   || ||||| ||   ||| ||||||||||     |||||  ||||
Db        102 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 161

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
               || |    |||||||||| | |||||  |    ||    ||  ||||    ||  | |
Db        162 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 221

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
              ||| | ||||||||||    || ||||||    | |||||  |||||||  |  | |   ||
Db        222 TGTCTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 278

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
              | |   |       ||||||| |||  |||   |||  | |||  ||||   |      ||
Db        279 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 338

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
              ||||||| |||||||  |     |||    |    |          ||||  | ||  |  ||
Db        339 CAACTACTGGAGGCTAGTGAGTTGGAGTCTCACAGTAAGGTCAAGCACAGTCCCTGGTGG 398

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
              || ||||| || ||||| ||  | |||||  |  ||||||  ||||  ||  |||   |||  |
Db        399 CCTTTATGCACTAAACGGCACCATAAACGCGGTGACCTTCCAAGGAAGCCTGAGTGAACT 458

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
              |       | | ||||||| |  |||||||    |||| | |||   | | ||||||  |
Db        459 GACAGATGTTAGCTACAACGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 518

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
              |||   || ||      |||| || || |||||  |   |||| |||   |  ||
Db        519 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATGTTGG 578

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
              || ||  | || |  |||   | ||||      || ||  |  |||  |  |  | || |
Db        579 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 638

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
                  |||  |           |      |           | |      | ||||
Db        639 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATAATTACCAATT 698

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              | | | |     |  |   ||    | ||| || | |   |  |||   ||
Db        699 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 758

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
              | |||        |  ||  ||||||  |    ||||        |  |||  |
Db        759 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAACAAGCGTCCAAAGCCTTGT 818

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
                |  |    |  || ||   | | |||    ||   ||       |  |  || |||
Db        819 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 878

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
              | |    ||      ||  ||||  |  |||||    |   | ||          |||
Db        879 GGCCGCAAACAATGGGCTGACGGCCGGCATCGACAATCTTATGCCATTCAATCTTGTGAT 938

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
              |               ||| ||  ||||||    | ||||    ||  |   || | |
Db        939 TCCAACCAATGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTC 995

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
              ||| |   |   ||| |||     || |  |  | ||   | ||||    ||  ||
Db        996 CAAAAGTGATGGTCAGGCAGG----GGAACAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1051

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
                | |      |  |        || ||    || || |  ||| | ||  |||||||
Db       1052 CAGTGACGATCCATGGT--------GGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1103

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
              |||||||| || |   || || |    ||  || | || || ||||| |||  |||||
Db       1104 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1163

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
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Db       1164 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATATGGCCGATTTGA 1223

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232

Db       1224 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCGCCTTGGCATCAA 1283

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292

Db       1284 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1343

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352

Db       1344 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1403

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACC 1403

Db       1404 AAGGAGGATAGCTGTACCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCC 1454


RESULT 10
US-07-944-943-1
; Sequence 1, Application US/07944943
; Patent No. 5518724
;  GENERAL INFORMATION:
;    APPLICANT:  SNYDER, DAVID B.
;    APPLICANT:  VAKHARIA, VIKRAM
;    TITLE OF INVENTION:  NOVEL INFECTIOUS BURSAL DISEASE VIRUS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/944,943
;      FILING DATE:  19920915
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kelber, Steven B.
;      REGISTRATION NUMBER:  30,073
;      REFERENCE/DOCKET NUMBER:  2284-029-0 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3180 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  64..3099
US-07-944-943-1

  Query Match             16.9%;  Score 239.2;  DB 2;  Length 3180;
  Best Local Similarity   50.6%;  Pred. No. 9.9e-56;
  Matches  695;  Conservative    0;  Mismatches  658;  Indels   21;  Gaps    4;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95

Db        114 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 173

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155

Db        174 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 233

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215

Db        234 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 290

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275

Db        291 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 350

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335

Db        351 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 410

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395

Db        411 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 470

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455

Db        471 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATCGG 530

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515

Db        531 GAACGTCCTAGTAGGGGAAGGGGTCACCGTCCTCAGCTTACCCACATCATATGATCTTGG 590

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572

Db        591 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 650

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632

Db        651 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATGATTACCAATT 710

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692

Db        711 CTCATCACAGTACCAATCAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 770

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752

Db        771 CATCACAAGCCTCAGCGTTGGGGGAGAGCTCGTGTTTAAAACAAGCGTCCAAAGCCTTGT 830

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812

Db        831 ACTGGGCGCCACCATCTACCTCATAGGCTTTGATGGGACTGCGGTAATCACTAGAGCTGT 890

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872

Db        891 GGCCGCGAACAATGGGCTGACGGCCGGCACCGACAATCTTATGCCATTCAATCTTGTGAT 950

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932

Db        951 -------TCCAACCAACGAGATAACCCAGCCAATCACATCCATCAAACTGAAGATTGTGA 1003

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992

Db       1004 CCTCCAAAAGTGGTGGTCTGGAAGGGGATCAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1063

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052

Db       1064 CAGTGACGATCCATGGT--------GGCAACTATCCAGGGGCCCTCCGTCCCGTCACACT 1115

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112

Db       1116 AGTAGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1175

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172

Db       1176 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1235
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Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
Db       1236 CCCAGGAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGCCTTGGCATCAA 1295

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
Db       1296 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1355

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
Db       1356 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1415

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
Db       1416 AAGGAGGATAGCTGTGCCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCCCCT 1469


RESULT 11
PCT-US91-03056-15
; Sequence 15, Application PC/TUS9103056
;  GENERAL INFORMATION:
;    APPLICANT:  Vakharia, Vikram
;    TITLE OF INVENTION:  SPECIFIC DNA AND RNA SEQUENCES
;    TITLE OF INVENTION:  ASSOCIATED WITH US IBDV VARIANTS, VECTOR CARRYING DNA
;    TITLE OF INVENTION:  SEQUENCES, HOST CARRYING CLONED VECTOR, DEDUCED AMINO ACID
;    TITLE OF INVENTION:  SEQUENCES, VACCINE AND METHOD OF VACCINATION
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;     ·ADDRESSEE:  Viviana Amzel, Ph.D.
;      STREET:  112 East Pecan, 2000 NBC Bank Plaza
;      CITY:  San Antonio
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  78205
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/03056
;      FILING DATE:  19910718
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/514,202
;      FILING DATE:  14-MAY-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Amzel Ph.D., Viviana
;      REGISTRATION NUMBER:  30,930
;      REFERENCE/DOCKET NUMBER:  U-0125.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/554-5325
;      TELEFAX:  512/226-8395
;      TELEX:  762609
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1471 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    ORIGINAL SOURCE:
;      ORGANISM:  Infectious bursal disease virus of chickens
;      STRAIN:  E/DEL
;     IMMEDIATE SOURCE:
;      CLONE:  E/DEL-2
PCT-US91-03056-15

  Query Match             16.9%;  Score 239;  DB 6;  Length 1471;
  Best Local Similarity   51.1%;  Pred. No. 8.3e-56;
  Matches  700;  Conservative    0;  Mismatches  650;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
Db        102 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 161

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
Db        162 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 221

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
Db        222 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 278

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
Db        279 CAATGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 338

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
Db        339 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 398

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
Db        399 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 458

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
Db        459 GACAGATGTTAGCTACAACGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 518

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
Db        519 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATCTTGG 578

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
Db        579 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 638

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
Db        639 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATAATTACCAATT 698

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
Db        699 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 758

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
Db        759 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAACAAGCGTCCAAAGCCTTGT 818

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
Db        819 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 878

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
Db        879 GGCCGCAAACAATGGGCTGACGGCCGGCATCGACAATCTTATGCCATTCAATCTTGTGAT 938

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
Db        939 TCCAACCAATGAGATAACCCAGCCAATCACA---TCCATCAAACTGGAGATAGTGACCTC 995

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
Db        996 CAAAAGTGATGGTCAGGCAGG----GGAACAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1051

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
Db       1052 CAGTGACGATCCATGGT--------GGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1103

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
Db       1104 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1163

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
Db       1164 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATATGGCCGATTTGA 1223
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Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
             ||| | ||   | |||||  | ||  |||| |||    | |||||    || | |||||
Db       1224 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCGCCTTGGCATCAA 1283

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
             ||| || |||   |||  |||||||| ||           |||||  ||  |  | ||
Db       1284 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1343

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
             | ||  |  |  ||||   |   ||  ||||  ||||  | ||||||| || | |  ||
Db       1344 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1403

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACC 1403
                |||   | || |  || ||  | || ||  |||| |||   || || ||
Db       1404 AAGGAGGATAGCTGTACCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCC 1454


RESULT 12
US-07-944-525-1
; Sequence 1, Application US/07944525
; Patent No. 5632989
;  GENERAL INFORMATION:
;    APPLICANT:  SNYDER, DAVID B.
;    APPLICANT:  VAKHARIA, VIKRAM
;    APPLICANT:  LUETTICKEN, HEINRICH D.
;    TITLE OF INVENTION:  ATTENUATED, LIVE VACCINE FOR DELAWARE
;    TITLE OF INVENTION:  STRAIN IBDV
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER AND
;      ADDRESSEE:  NEUSTADT, P.C.
;      STREET:  1755 JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/944,525
;      FILING DATE:  19920914
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KELBER, STEVEN B.
;      REGISTRATION NUMBER:  30,073
;      REFERENCE/DOCKET NUMBER:  2284-028-0 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3180 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  64..3099
US-07-944-525-1

  Query Match             16.9%;  Score 238.8;  DB 2;  Length 3180;
  Best Local Similarity   51.0%;  Pred. No. 1.3e-55;
  Matches  701;  Conservative    0;  Mismatches  652;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
              | |  || | |||   || ||||| ||   ||| ||||||||||    |||||  ||||
Db        114 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 173

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
              || |    |||||||||| | |||||  |    ||    ||  ||||    ||  |  |
Db        174 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 233

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
              ||| | |||||||||    || ||||||    | |||||  ||||||  |  | |   ||
Db        234 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 290

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
              |      |       |||||||  |||  |||   |||  | |||  ||||    |      ||
Db        291 CAGTGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 350

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
              |||||||  | |||||  |     |||     |     |          ||||||  ||  |  ||
Db        351 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 410

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
              | ||||| || ||||| ||  | |||||  |  ||||||  |||| || |||  |||  |
Db        411 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 470

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
              |       | | |||||||  |||||||   |||| | |||  | | ||||||  |
Db        471 GACAGATGTTAGCTACAACGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 530

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
              |||   || ||      |||| || || ||||| |    |||| |||    |  ||
Db        531 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATCTTGG 590

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
              || ||  | || |  |||   | ||||     || ||  |  |||  |  |  || |
Db        591 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 650

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
                  |||  |                |      |          | |      | ||||
Db        651 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATAATTACCAATT 710

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
              |  | | |       |  |    ||       | ||| || | |   |  |||   ||
Db        711 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 770

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
              | |||       |  ||  ||||||  |   ||||       |  |||  |
Db        771 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAACAAGCGTCCAAAGCCTTGT 830

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
              |  |      |  || ||   | | |||    ||   ||        |  |  || |||
Db        831 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 890

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
              | |    ||      ||  ||||   | |||||     |    | ||         |||
Db        891 GGCCGCAAACAATGGGCTGACGGCCGGCATCGACAATCTTATGCCATTCAATCTTGTGAT 950

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
              |       ||| ||  ||||||   | ||||    ||  |  || | |
Db        951 TCCAACCAATGAGATAACCCAGCCAATCACA---TCCATCATACTGGAGATAGTGACCTC 1007

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
              |||  |   |  ||| |||     || |  |  | ||   | ||||    ||  ||
Db       1008 CAAAAGTGATGGTCAGGCAGG----GGAACAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1063

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
              |  |      |  |       || ||    || || |  ||| | ||  |||||||
Db       1064 CAGTGACGATCCATGGT--------GGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1115

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
              |||||||| || |  || || |   ||  || | || || ||||| |||  |||||
Db       1116 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1175

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
              |||||||||||||| || |||||    |||||| |||| |||   || |||    |  ||
Db       1176 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1235
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Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
Db       1236 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCACCTTGGCATCAA 1295

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
Db       1296 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1355

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
Db       1356 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1415

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
Db       1416 AAGGAGGATAGCTGTACCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCCTCT 1469


RESULT 13
US-08-219-262B-13
; Sequence 13, Application US/08219262B
; Patent No. 5788970
;  GENERAL INFORMATION:
;    APPLICANT:  VAKHARIA, VIKRAM
;    APPLICANT:  SNYDER, DAVID B
;    APPLICANT:  MENGEL-WHERSAT, STEPHANIE A
;    TITLE OF INVENTION:  CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
;    TITLE OF INVENTION:  cDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
;    TITLE OF INVENTION:  THEREON
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
;      STREET:  1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/219,262B
;      FILING DATE:  29-MAR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  2747-047-27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3180 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  64..3099
US-08-219-262B-13

  Query Match           16.9%;  Score 238.8;  DB 2;  Length 3180;
  Best Local Similarity   51.0%;  Pred. No. 1.3e-55;
  Matches  701;  Conservative    0;  Mismatches  652;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95
Db        114 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 173

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
Db        174 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 233

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
Db        234 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 290

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
Db        291 CAGTGGGAACTACAAGTTCGATCAGATGCTCCTGACTGCCCAGAACCTACCGGCCAGCTA 350

Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
Db        351 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 410

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
Db        411 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 470

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
Db        471 GACAGATGTTAGCTACAACGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 530

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
Db        531 GAACGTCCTAGTAGGGGAAGGGGTAACCGTCCTCAGCTTACCCACATCATATGATCTTGG 590

Qy        516 ATACGTCCGCCTAGAGGACGAGACACCC---CAGGGTCTCCAGTCAATGAACGGGGCCAA 572
Db        591 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 650

Qy        573 GATGAGGTGCACAGCTGCAATTGCACCGCGGAGGTACGAGATCGACCTCCCATCCCAACG 632
Db        651 ATGTGACAGCAGTGACAGGCCCAGAGTCTACACCATAACTGCAGCCGATAATTACCAATT 710

Qy        633 CCTACCCCCCGTTCCTGCGACAGGAACCCTCACCACTCTCTACGAGGGAAACGCCGACAT 692
Db        711 CTCATCACAGTACCAAACAGGTGGGGTAACAATCACACTGTTCTCAGCCAACATTGATGC 770

Qy        693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752
Db        771 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAACAAGCGTCCAAAGCCTTGT 830

Qy        753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812
Db        831 ACTGGGCGCCACCATCTACCTTATAGGCTTTGATGGGACTGCGGTAATCACCAGAGCTGT 890

Qy        813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872
Db        891 GGCCGCAAACAATGGGCTGACGGCCGGCATCGACAATCTTATGCCATTCAATCTTGTGAT 950

Qy        873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932
Db        951 TCCAACCAATGAGATAACCCAGCCAATCACA---TCCATCATACTGGAGATAGTGACCTC 1007

Qy        933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992
Db       1008 CAAAAGTGATGGTCAGGCAGG----GGAACAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1063

Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
Db       1064 CAGTGACGATCCATGGT--------GGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1115

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
Db       1116 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1175

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
Db       1176 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1235

Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
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Db       1236 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCACCTTGGCATCAA 1295

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292

Db       1296 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1355

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352

Db       1356 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1415

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406

Db       1416 AAGGAGGATAGCTGTACCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCCTCT 1469


RESULT 14
US-09-031-655-13
; Sequence 13, Application US/09031655
; Patent No. 6017759
;  GENERAL INFORMATION:
;    APPLICANT:  VAKHARIA, VIKRAM
;    APPLICANT:  SNYDER, DAVID B
;    APPLICANT:  MENGEL-WHERSAT, STEPHANIE A
;    TITLE OF INVENTION:  CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
;    TITLE OF INVENTION:  cDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
;    TITLE OF INVENTION:  THEREON
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
;      STREET:  1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/031,655
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/219,262
;      FILING DATE:  29-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  2747-047-27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3180 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  64..3099
US-09-031-655-13

  Query Match             16.9%;  Score 238.8;  DB 3;  Length 3180;
  Best Local Similarity   51.0%;  Pred. No. 1.3e-55;
  Matches  701;  Conservative    0;  Mismatches  652;  Indels   21;  Gaps    5;

Qy         36 CATCATGCTTCCAGAGACTGGACCAGCAAGCATCCCGGACGACATAACGGAGAGACACAT 95

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Qy        96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155

Db       174 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 233

Qy       156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215

Db       234 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 290

Qy       216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275

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Qy       276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335

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Db       411 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 470

Qy       396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455

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Db       591 GTATGTGAGGCTTGGTGACCCCATACCCGCTATAGGGCTTGACCCAAAAATGGTAGCAAC 650

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Qy       693 CGTCAACTCCACAACAGTGACGGGAGACATAAACTTCAGTCTGGCAGAACAACCCGCAAA 752

Db       771 CATCACAAGTCTCAGCGTTGGGGGAGAGCTCGTGTTCAAAACAAGCGTCCAAAGCCTTGT 830

Qy       753 CGAGACCAAGTTCGACTTCCAGCTGGACTTCATGGGCCTTGACAACGACGTCCCAGTTGT 812

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Qy       813 CACAGTGGTCAGCTCCGTGCTGGCCACAAATGACAACTACAGAGGAGTCTCAGCCAAGAT 872

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Qy       873 GACCCAGTCCATCCCGACCGAGAACATCACAAAGCCGATCACCAGGGTCAAGCTGTCATA 932

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Qy       933 CAAGATCAACCAGCAGACAGCAATCGGCAACGTCGCCACCCTGGGCACAATGGGTCCAGC 992

Db      1008 CAAAAGTGATGGTCAGGCAGG----GGAACAGATGTCATGGTCGGCAAGTGGGAGCCTAG 1063

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Db      1064 CAGTGACGATCCATGGT--------GGCAACTATCCAGGAGCCCTCCGTCCCGTCACACT 1115

Qy      1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112

Db      1116 AGTGGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1175

Qy      1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172

Db      1176 CGAGCTGATCCCAAATCCTGAACTAGCAAAGAACCTGGTTACAGAATACGGCCGATTTGA 1235
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Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
Db       1236 CCCAGGAGCCATGAACTACACGAAATTGATACTGAGTGAGAGGGACCACCTTGGCATCAA 1295

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
Db       1296 GACCGTCTGGCCAACAAGGGAGTACACTGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1355

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
Db       1356 CCTCAACTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1415

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
Db       1416 AAGGAGGATAGCTGTACCGGTGGTCTCTACATTGTTCCCACCTGCCGCTCCTCT 1469


RESULT 15
US-08-219-262B-11
; Sequence 11, Application US/08219262B
; Patent No. 5788970
;  GENERAL INFORMATION:
;    APPLICANT:  VAKHARIA, VIKRAM
;    APPLICANT:  SNYDER, DAVID B
;    APPLICANT:  MENGEL-WHERSAT, STEPHANIE A
;    TITLE OF INVENTION:  CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
;    TITLE OF INVENTION:  cDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
;    TITLE OF INVENTION:  THEREON
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
;      STREET:  1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/219,262B
;      FILING DATE:  29-MAR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  2747-047-27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3230 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  114..3149
US-08-219-262B-11

  Query Match           16.8%;  Score 237.2;  DB 2;  Length 3230;
  Best Local Similarity  50.9%;  Pred. No. 3.6e-55;
  Matches  700;  Conservative    0;  Mismatches  653;  Indels   21;  Gaps    5;

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Db        164 CCTTCTGATGCCAACAACCGGACCGGCGTCCATTCCGGACGACACCCTGGAGAAGCACAC 223

Qy         96 CCTAAAACAAGAGACCTCGTCATACAACCTAGAGGTCTCCGAATCAGGAAGTGGCATTCT 155
Db        224 TCTCAGGTCAGAGACCTCGACCTACAATTTGACTGTGGGGGACACAGGGTCAGGGCTAAT 283

Qy        156 TGTTTGTTTCCCTGGGGCACCAGGCTCACGGATCGGTGCACACTACAGATGGAATGCGAA 215
Db        284 TGTCTTTTTCCCTGGATTCCCTGGCTCAATTGTGGGTGCTCACTACACACTGCA---GAG 340

Qy        216 CCAGACGGGGCTGGAGTTCGACCAGTGGCTGGAGACGTCGCAGGACCTGAAGAAAGCCTT 275
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Qy        276 CAACTACGGGAGGCTGATCTCAAGGAAATACGACATCCAAAGCTCCACACTACCGGCCGG 335
Db        401 CAACTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTAAGGTCAAGCACACTCCCTGGTGG 460

Qy        336 TCTCTATGCTCTGAACGGGACGCTCAACGCTGCCACCTTCGAAGGCAGTCTGTCTGAGGT 395
Db        461 CGTTTATGCACTAAACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACT 520

Qy        396 GGAGAGCCTGACCTACAACAGCCTGATGTCCCTAACAACGAACCCCCAGGACAAAGTCAA 455
Db        521 GACAGATGTTAGCTACAATGGGTTGATGTCTGCAACAGCCAACATCAACGACAAAATTGG 580

Qy        456 CAACCAGCTGGTGACCAAAGGAGTCACAGTCCTGAATCTACCAACAGGGTTCGACAAACC 515
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Qy        993 ATCCGTCTCCTTCTCATCAGGGAACGGAAATGTCCCCGGCGTGCTCAGACCAATCACACT 1052
Db       1114 CAGTGACGATTCATGGT--------GGCAACTATCCAGGGGCCCTCCGTCCCGTCACACT 1165

Qy       1053 GGTGGCCTATGAGAAGATGACACCGCTGTCCATCCTGACCGTAGCTGGAGTGTCCAACTA 1112
Db       1166 AGTAGCCTACGAAAGAGTGGCAACAGGATCTGTCGTTACGGTCGCTGGGGTGAGCAACTT 1225

Qy       1113 CGAGCTGATCCCAAACCCAGAACTCCTCAAGAACATGGTGACACGCTATGGCAAGTACGA 1172
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Qy       1173 CCCCGAAGGTCTCAACTATGCCAAGATGATCCTGTCCCACAGGGAAGAGCTGGACATCAG 1232
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Db       1286 CCCAGGAGCCATGAACTACACAAAATTGATACTGAGTGAGAGGGACCGCCTTGGCATCAA 1345

Qy       1233 GACAGTGTGGAGGACAGAGGAGTACAAGGAGAGGACCAGAGTCTTCAACGAAATCACGGA 1292
              |||||| |||  ||||  |||||||| ||             |||||  ||  |  | ||
Db       1346 GACAGTCTGGCCGACAAGGGAGTACACCGACTTTCGTGAGTACTTCATGGAGGTGGCCGA 1405

Qy       1293 CTTCTCCAGTGACCTGCCCACGTCAAAGGCATGGGGCTGGAGAGACATAGTCAGAGGAAT 1352
              | ||  |  |  ||||  |   ||   ||||  ||||  | ||||||| || | |  ||
Db       1406 CCTCAGCTCTCCCCTGAAGATTGCAGGAGCATTTGGCTTCAAAGACATAATCCGGGCCAT 1465

Qy       1353 TCGGAAAGTCGCAGCTCCTGTACTGTCCACGCTGTTTCCAATGGCAGCACCACT 1406
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